

> 0 <
01 10 Intelligenetics
> 0 <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "seq127c-pen" --

Selected search type is key against sequence data banks or files.

Selected scope is sequence. "09-883727.key":

Selected sequence key from "09-883727.key":
seq127c (AA) ID seq127c AA preliminary pattern
followed by
1 pn
2 any character
2 any character
2 y
2 any character
2 any character
2 any character
2 any character
2 any character
2 y
2 any character
2 any character
2 any character
2 any character
2 y
2 any character
2 any character
2 any character
2 any character
2 any character
2 any character
2 any character

Selected data banks and files:

Data bank : Pending_AA , all entries

-- Output Parameters --

Format Options:	File Options:
Nucleic acid code matching	Exact
Find non-matching hits only	No
Report key used	Yes
Note position of hit	Yes
Display full annotations	Yes
Sequence context	50

-- Run Parameters --

Run mode	Batch
Time to start comparison	NO
Notify at end of run	NO

1 match found in sequence:

US-08-827-356-5380 : Sequence 5380, Application US/08827356
(from "/src/h/paa/US088_COMB.pep")
Sequence 5380, Application US/08827356

GENERAL INFORMATION:

APPLICANT: George H. Shimer, Jr.

APPLICANT: George H. Miller

APPLICANT: Roberta S. Hare

APPLICANT: Karen J. Shaw

TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS RELATED

NUMBER OF SEQUENCES: 5574

CORRESPONDENCE ADDRESS:

STREET: 2000 Galloping Hill Road
CITY: Kenilworth

STATE: New Jersey

COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentlin

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/827,356

FILING DATE: 01-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/014,477

FILING DATE: 01-APR-1996

APPLICATION NUMBER: 60/016,743

FILING DATE: 02-MAY-1996

APPLICATION NUMBER: 60/020,016

FILING DATE: 14-JUN-1996

INFORMATION FOR SEQ ID NO: 5380:

SEQUENCE CHARACTERISTICS:

LENGTH: 313 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Staphylococcus aureus

FEATURE:

NAME/KEY: misc-feature

LOCATION: 1...313

Found using 'seq127c' (09-883727.key)

215 ISSHHHHHGKISMTYFTGPIIDROLFYQITMKLPESVLRKGYSPFNQNAIYEPQYA
265

275 YGLPDYGIIGMOLPLTIYIGETLDTNHIHQDLMLQPT
284

1 match found in sequence:

US-09-417-507-32518 : Sequence 32518, Application US/09417507
(from "/src/h/paa/US094_COMB.pep")
Sequence 32518, Application US/09417507

GENERAL INFORMATION:

APPLICANT: KEITH G. WEINSTOCK ET AL.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS

TITLE OF INVENTION: FUMIGATUS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: PATH99-10

CURRENT APPLICATION NUMBER: US/09/417,507

CURRENT FILING DATE: 1999-10-14

NUMBER OF SEQ ID NOS: 44312

SEQ ID NO 32518

LENGTH: 280

TYPE: PRT

ORGANISM: A. fumigatus

Found using 'seq127c' (09-883727.key)

6 RNLHRTGMRFPQARSQVELFHHVLELATVKKHVRSHHPLATPNDIYAESPSNFVTDNH
56

66 YRREGYGLIEDLIPAAKWSIVVLIQDLKSKADKGIDATVALTGILHNNNGIGHGRSK
75

1 match found in sequence:
 US-09-478-081-783 ; Sequence 783, Application US/09478081
 (from "/srch/paa/US094_COMB.pep")
 Sequence 783, Application US/09478081
 GENERAL INFORMATION:
 APPLICANT: ALEXANDROV, Nikolai
 APPLICANT: CHEN, Xianfeng
 APPLICANT: SUBRAMANIAN, Gopalakrishnan
 APPLICANT: ZHENG, Liansheng
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS 60-61, 67, 69, 71-80,
 FILE REFERENCE: 2750-683P
 CURRENT APPLICATION NUMBER: US/09/478,081
 CURRENT FILING DATE: 2000-01-04
 NUMBER OF SEQ ID NOS: 1052
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 783
 LENGTH: 131
 TYPE: PRP
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 OTHER INFORMATION: any n or Xaa = unknown
 Found using 'seq127c' (09-883727.key)

1 VRLCEKAKELIMNESNVQPYKSPVITICGNHGFHNLAEFRIGCMCPNTNYLFKGNVY

 61 NRGYSVEVTLLVALKMRYPORITILRGHNSROIYQVYGFYNECLRKYGANANWKI
 68

1 match found in sequence:
 US-09-513-996A-55619 ; Sequence 55619, Application US/09513996A
 (from "/srch/paa/US095_COMB.pep")
 Sequence 55619, Application US/09513996A
 GENERAL INFORMATION:
 APPLICANT: N. ALEXANDROV et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 TITLE OF INVENTION: ENCODED THEREBY
 FILE REFERENCE: 2750-709P
 CURRENT APPLICATION NUMBER: US/09/513,996A
 CURRENT FILING DATE: 2000-02-25
 NUMBER OF SEQ ID NOS: 81028
 SEQ ID NO 55619
 LENGTH: 193
 TYPE: PRP
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: UNSURE
 LOCATION: 1..193
 OTHER INFORMATION: any n or Xaa = unknown
 FEATURE:
 OTHER INFORMATION: Location 1..193 / Ceres Seq. ID 2113886
 Found using 'seq127c' (09-883727.key)

1 MPYTISSPTLKRLSVHYEHFESVISFDLPNLEYLDYSYALYGYPOVNESEIVEAYINT

 61 DKAHVESPDVTKLIMGIRNVEILSLSPDSVGYIYSCK
 30
 49
 1 match found in sequence:
 US-09-513-996A-66072 ; Sequence 66072, Application US/09513996A
 (from "/srch/paa/US095_COMB.pep")
 Sequence 66072, Application US/09513996A
 GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE
 TITLE OF INVENTION: ENCODED THEREBY
 FILE REFERENCE: 2750-709P
 CURRENT APPLICATION NUMBER: US/09/513,996A
 CURRENT FILING DATE: 2000-02-25
 NUMBER OF SEQ ID NOS: 81028
 SEQ ID NO 66072
 LENGTH: 403
 TYPE: PRP
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: UNSURE
 LOCATION: 1..403
 OTHER INFORMATION: any n or Xaa = unknown
 FEATURE:
 OTHER INFORMATION: Location 1..403 / Ceres Seq. ID 2172330
 Found using 'seq127c' (09-883727.key)

190 NVLLACPVVEALYLNONGESMPYTISSPTLKRLSVHYEHFESVISFDLPNLEYLDYS

 250 YALYGYPOVNESEIVEAYNLDKAHSVSPDVTKLIMGIRNVEILSLSPDSVGYIYSCK
 259
 240

1 match found in sequence:
 US-09-513-996A-66073 ; Sequence 66073, Application US/09513996A
 (from "/srch/paa/US095_COMB.pep")
 Sequence 66073, Application US/09513996A
 GENERAL INFORMATION:
 APPLICANT: N. ALEXANDROV et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE
 TITLE OF INVENTION: ENCODED THEREBY
 FILE REFERENCE: 2750-709P
 CURRENT APPLICATION NUMBER: US/09/513,996A
 CURRENT FILING DATE: 2000-02-25
 NUMBER OF SEQ ID NOS: 81028
 SEQ ID NO 66073
 LENGTH: 341
 TYPE: PRP
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: UNSURE
 LOCATION: 1..341
 OTHER INFORMATION: any n or Xaa = unknown
 FEATURE:
 OTHER INFORMATION: Location 1..341 / Ceres Seq. ID 2172331
 Found using 'seq127c' (09-883727.key)

128 NVLLACPVVEALYLNONGESMPYTISSPTLKRLSVHYEHFESVISFDLPNLEYLDYS

 188 YALYGYPOVNESEIVEAYNLDKAHSVSPDVTKLIMGIRNVEILSLSPDSVGYIYSCK
 197

1 match found in sequence:
 US-09-573-655A-695 ; Sequence 695, Application US/09573655A
 (from "/srch/paa/US095_COMB.pep")
 Sequence 695, Application US/09573655A

GENERAL INFORMATION:

APPLICANT: SOLOVEY, Victor and TROUKHAN, Maxim
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 TITLE OF INVENTION: Thereby
 FILE REFERENCE: 2750-0876P
 CURRENT APPLICATION NUMBER: US/09/573,655A
 CURRENT FILING DATE: 2000-05-18
 NUMBER OF SEQ ID NOS: 3280
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 695
 LENGTH: 882
 TYPE: PRF
 ORGANISM: Arabidopsis thaliana
 Found using 'seq127c' (09-883727.key)

575 NLLAGCPVEALYLNONGESMPYTISSPTLKRSLVHYEHFESVISFDLPNLEYLYSD 625

635 YALGYQVNEISLVEAYLNLDKAHVESPDYTKLIMGIRNVEILSLSPDSVGVIYSCK 644

1 match found in sequence:

US-09-573-655A-1048 ; Sequence 1048, Application US/09573655A
 (from "/srch/paa/US095_COMB.pep")
 Sequence 1048, Application US/09573655A

GENERAL INFORMATION:

APPLICANT: SOLOVEY, Victor and TROUKHAN, Maxim
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 TITLE OF INVENTION: Thereby
 FILE REFERENCE: 2750-0876P
 CURRENT APPLICATION NUMBER: US/09/573,655A
 CURRENT FILING DATE: 2000-05-18
 NUMBER OF SEQ ID NOS: 3280
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 1048
 LENGTH: 882
 TYPE: PRF
 ORGANISM: Arabidopsis thaliana
 Found using 'seq127c' (09-883727.key)

575 NLLAGCPVEALYLNONGESMPYTISSPTLKRSLVHYEHFESVISFDLPNLEYLYSD 625

635 YALGYQVNEISLVEAYLNLDKAHVESPDYTKLIMGIRNVEILSLSPDSVGVIYSCK 644

1 match found in sequence:

US-09-573-655A-1078 ; Sequence 1078, Application US/09573655A
 (from "/srch/paa/US095_COMB.pep")
 Sequence 1078, Application US/09573655A

GENERAL INFORMATION:

APPLICANT: SOLOVEY, Victor and TROUKHAN, Maxim
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 TITLE OF INVENTION: Thereby
 FILE REFERENCE: 2750-0876P
 CURRENT APPLICATION NUMBER: US/09/573,655A
 CURRENT FILING DATE: 2000-05-18
 NUMBER OF SEQ ID NOS: 3280
 SOFTWARE: PatentIn version 3.0

SEQ ID NO: 1078

LENGTH: 407

TYPE: PRF

ORGANISM: Arabidopsis thaliana

Found using 'seq127c' (09-883727.key)

125 DTISIGKAGISDNVYFDFTNRVSYSKTFKRLKLCIDYDQNPDTVSFDTNLEYLYSD 175

185 YVAVKYPRVFCSLVEASLNLQMTYDQCAQASYGFLVGNATDFLMGVSNQVLIHLSDKSL 194

1 match found in sequence:

US-09-573-655A-1768 ; Sequence 1768, Application US/09573655A
 (from "/srch/paa/US095_COMB.pep")
 Sequence 1768, Application US/09573655A

GENERAL INFORMATION:

APPLICANT: SOLOVEY, Victor and TROUKHAN, Maxim
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 TITLE OF INVENTION: Thereby
 FILE REFERENCE: 2750-0876P
 CURRENT APPLICATION NUMBER: US/09/573,655A
 CURRENT FILING DATE: 2000-05-18
 NUMBER OF SEQ ID NOS: 3280
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 1768
 LENGTH: 882
 TYPE: PRF
 ORGANISM: Arabidopsis thaliana
 Found using 'seq127c' (09-883727.key)

575 NLLAGCPVEALYLNONGESMPYTISSPTLKRSLVHYEHFESVISFDLPNLEYLYSD 625

635 YALGYQVNEISLVEAYLNLDKAHVESPDYTKLIMGIRNVEILSLSPDSVGVIYSCK 644

1 match found in sequence:

US-09-573-655B-695 ; Sequence 695, Application US/09573655B
 (from "/srch/paa/US095_COMB.pep")
 Sequence 695, Application US/09573655B

GENERAL INFORMATION:

APPLICANT: SOLOVEY, Victor and TROUKHAN, Maxim
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 TITLE OF INVENTION: Thereby
 FILE REFERENCE: 2750-0876P
 CURRENT APPLICATION NUMBER: US/09/573,655B
 CURRENT FILING DATE: 2000-05-18
 NUMBER OF SEQ ID NOS: 3281
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 695
 LENGTH: 882
 TYPE: PRF
 ORGANISM: Arabidopsis thaliana
 Found using 'seq127c' (09-883727.key)

575 NLLAGCPVEALYLNNGESMPYTISSPTLKRLSVHYEHFESVISFDLPNLEYLDYSD
625

635 YALXGYQVNLSEIVEAYLNLDKAEHVESPDVTKLIMGIRNVEILSLSPDSVGVIYSCK
644

1 match found in sequence:

US-09-573-655B-1048 ; Sequence 1048, Application US/09573655B

(from "/src/paa/US095_COMB.pep")

Sequence 1048, Application US/09573655B

GENERAL INFORMATION:

APPLICANT: SOLOVYEV, Victor and TROUKHAN, Maxim

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

FILE REFERENCE: 2750-0876P

CURRENT APPLICATION NUMBER: US/09/573,655B

CURRENT FILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 3281

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1048

LENGTH: 882

TYPE: PRT

ORGANISM: Arabidopsis thaliana

Found using 'seq127c' (09-883727.key)

575 NLLAGCPVEALYLNNGESMPYTISSPTLKRLSVHYEHFESVISFDLPNLEYLDYSD
625

635 YALXGYQVNLSEIVEAYLNLDKAEHVESPDVTKLIMGIRNVEILSLSPDSVGVIYSCK
644

1 match found in sequence:

US-09-573-655B-1078 ; Sequence 1078, Application US/09573655B

(from "/src/paa/US095_COMB.pep")

Sequence 1078, Application US/09573655B

GENERAL INFORMATION:

APPLICANT: SOLOVYEV, Victor and TROUKHAN, Maxim

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

FILE REFERENCE: 2750-0876P

CURRENT APPLICATION NUMBER: US/09/573,655B

CURRENT FILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 3281

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1078

LENGTH: 407

TYPE: PRT

ORGANISM: Arabidopsis thaliana

Found using 'seq127c' (09-883727.key)

125 DTISGKAGIGSDNVYFDFTNRSVSKTFRKLKLCIDYDQNPDTVSFDLPNLEYLDYSD
175

185 YVAVKYPVRFECSLVEASLNLQMTYDCAQASVGYFLVGNATDPLMGVSNVQILHLSDKSL
194

1 match found in sequence:

US-09-573-655B-1768 ; Sequence 1768, Application US/09573655B

(from "/src/paa/US095_COMB.pep")

Sequence 1768, Application US/09573655B

GENERAL INFORMATION:

APPLICANT: SOLOVYEV, Victor and TROUKHAN, Maxim

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide

FILE REFERENCE: 2750-0876P

CURRENT APPLICATION NUMBER: US/09/573,655B

CURRENT FILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 3281

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1768

LENGTH: 882

TYPE: PRT

ORGANISM: Arabidopsis thaliana

Found using 'seq127c' (09-883727.key)

575 NLLAGCPVEALYLNNGESMPYTISSPTLKRLSVHYEHFESVISFDLPNLEYLDYSD
625

635 YALXGYQVNLSEIVEAYLNLDKAEHVESPDVTKLIMGIRNVEILSLSPDSVGVIYSCK
644

1 match found in sequence:

US-09-595-332A-1615 ; Sequence 1615, Application US/09595332A

(from "/src/paa/US095_COMB.pep")

Sequence 1615, Application US/09595332A

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nikolai

APPLICANT: BROVER, Vyacheslav

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide

FILE REFERENCE: 2750-0949P

CURRENT APPLICATION NUMBER: US/09/595,332A

CURRENT FILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 1915

SEQ ID NO 1615

LENGTH: 194

TYPE: PRT

ORGANISM: Arabidopsis thaliana

FEATURE:

NAME/KEY: misc.feature

LOCATION: 1..194

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc.feature

LOCATION: 1..194

OTHER INFORMATION: Ceres Seq. ID 1015000

Found using 'seq127c' (09-883727.key)

1 MPTIISPTLKRLSVHYEHFESVISFDLPNLEYLDYSDYALYGYQVNLSEIVEAYLNL
30

61 DKAHVESPDVTKLIMGIRNVEILSLSPDSVGVIYSCK
49

1 match found in sequence:

US-09-611-529-4809 ; Sequence 4809, Application US/09611529

(from "/src/paa/US096_COMB.pep")

Sequence 4809, Application US/09611529

GENERAL INFORMATION:

*APPLICANT: George H. Shimer, Jr.
 APPLICANT: George H. Miller
 APPLICANT: Roberta S. Hare
 APPLICANT: Karen J. Shaw
 TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
 FILE REFERENCE: 1034/IC96J051
 CURRENT APPLICATION NUMBER: US/09/611,529
 CURRENT FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/417,811
 PRIOR FILING DATE: 1999-10-14
 PRIOR APPLICATION NUMBER: US 09/353,718
 PRIOR FILING DATE: 1999-07-14
 PRIOR APPLICATION NUMBER: US 09/266,557
 PRIOR FILING DATE: 1999-03-11
 PRIOR APPLICATION NUMBER: US 09/266,556
 PRIOR FILING DATE: 1999-03-11
 PRIOR APPLICATION NUMBER: US 09/266,555
 PRIOR FILING DATE: 1999-03-11
 PRIOR APPLICATION NUMBER: US 09/266,542
 PRIOR FILING DATE: 1999-03-11
 PRIOR APPLICATION NUMBER: US 09/266,541
 PRIOR FILING DATE: 1999-03-11
 PRIOR APPLICATION NUMBER: US 09/037,934
 PRIOR FILING DATE: 1998-03-10
 PRIOR APPLICATION NUMBER: US 09/036,720
 PRIOR FILING DATE: 1998-03-06
 PRIOR APPLICATION NUMBER: US 09/036,338
 PRIOR FILING DATE: 1998-03-06
 PRIOR APPLICATION NUMBER: US 09/036,334
 PRIOR FILING DATE: 1998-03-06
 PRIOR APPLICATION NUMBER: US 09/036,221
 PRIOR FILING DATE: 1998-03-06
 PRIOR APPLICATION NUMBER: US 09/036,137
 PRIOR FILING DATE: 1998-03-06
 PRIOR APPLICATION NUMBER: US 09/036,082
 PRIOR FILING DATE: 1998-03-06
 PRIOR APPLICATION NUMBER: US 09/036,081
 PRIOR FILING DATE: 1998-03-06
 PRIOR APPLICATION NUMBER: US 09/036,079
 PRIOR FILING DATE: 1998-03-06
 PRIOR APPLICATION NUMBER: US 09/035,913
 PRIOR FILING DATE: 1998-03-06
 PRIOR APPLICATION NUMBER: US 09/035,744
 PRIOR FILING DATE: 1998-03-06
 PRIOR APPLICATION NUMBER: US 08/827,356
 PRIOR FILING DATE: 1997-04-01
 PRIOR APPLICATION NUMBER: US 08/831,156
 PRIOR FILING DATE: 1997-04-01
 PRIOR APPLICATION NUMBER: US 60/014,477
 PRIOR FILING DATE: 1996-04-01
 PRIOR APPLICATION NUMBER: US 60/016,743
 PRIOR FILING DATE: 1996-05-02
 PRIOR APPLICATION NUMBER: US 60/020,016
 PRIOR FILING DATE: 1996-06-14
 NUMBER OF SEQ ID NOS: 7451
 SEQ ID NO 4809
 LENGTH: 313
 TYPE: PRT
 ORGANISM: Staphylococcus aureus
 Found using 'seq127c' (09-883727.key)

215 ISSHHHHHGIKSMYTFPTGPIIDROLFYQFIIMKLPESVLRKGYVSFPMQNSNAIYEPQY

 265

275 YGLPDYGIIGMQLPLTIVIGETILDTNHRNQLDMLQFT

 284

I match found in sequence:

US-09-688-051-1400 ; Sequence 1400, Application US/09688051
 (from "/src/h/paa/US096.COMB.pep")
 General 1400, Application US/09688051
 GENERAL INFORMATION:
 APPLICANT: ALEXANDROV, Nikolai
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
 TITLE OF INVENTION: Thereby
 FILE REFERENCE: 2750-1242P
 CURRENT APPLICATION NUMBER: US/09/688,051
 CURRENT FILING DATE: 2000-10-13
 NUMBER OF SEQ ID NOS: 4193
 SEQ ID NO 1400
 LENGTH: 193
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1..193
 OTHER INFORMATION: Xaa is any amino acid
 NAME/KEY: misc_feature
 LOCATION: 1..193
 OTHER INFORMATION: Ceres Seq. ID 1715644
 Found using 'seq127c' (09-883727.key)

1 MPYISSPTLRSLVHYEXHFESVISFDLPNLEYIDSDYALYGPQVNLSEIVEATYNTL

 30
 61 DKAEHVESPDVTKLIMGIRNVEILSLSPDSVGVIYSCKK

 1 match found in sequence:
 US-09-708-427-4276 ; Sequence 4276, Application US/09708427
 (from "/src/h/paa/US097.COMB.pep")
 Sequence 4276, Application US/09708427
 GENERAL INFORMATION:
 APPLICANT: N. ALEXANDROV et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE
 TITLE OF INVENTION: THEREBY
 FILE REFERENCE: 2750-1243P
 CURRENT APPLICATION NUMBER: US/09/708,427
 CURRENT FILING DATE: 2000-11-09
 NUMBER OF SEQ ID NOS: 85364
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 4276
 LENGTH: 737
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1..737
 OTHER INFORMATION: Xaa is any amino acid
 NAME/KEY: misc_feature
 LOCATION: 1..737
 OTHER INFORMATION: Ceres Seq. ID 1811913
 Found using 'seq127c' (09-883727.key)

183 GTLSRCPLVLELIVEERRCYDWCSSVSPSLKRLHIFDRKFTSISLDAENLIYKKHSG

 233

243 YVLGYPNVKLDLSLEARLNLMDETRMVGVNGSLGSIADMRNLINGIRNVRILHLS

 252

I match found in sequence:

1 match found in sequence:
US-09-708-427-4277 ; Sequence 4277, Application US/09708427
(from "/srch/paa/US097_COMB.pep")
Sequence 4277, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4277
LENGTH: 698
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..698
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc-feature
LOCATION: 1..698
OTHER INFORMATION: Ceres Seq. ID 1811914
Found using 'seq127c' (09-883727.key)

144 GTLISRCPLVEELVEERCVDMTCVSSPSLKRHLIRFDRKFTSLDAPNLIYYHSG
194

204 YVYGKYPNVRLDSLIEARLNLRMDETRMGVNRGSLGSPADMRNLINGIRNVRILHLS
213

1 match found in sequence:
US-09-708-427-4278 ; Sequence 4278, Application US/09708427
(from "/srch/paa/US097_COMB.pep")
Sequence 4278, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4278
LENGTH: 668
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..668
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc-feature
LOCATION: 1..668
OTHER INFORMATION: Ceres Seq. ID 1811915
Found using 'seq127c' (09-883727.key)

114 GTLISRCPLVEELVEERCVDMTCVSSPSLKRHLIRFDRKFTSLDAPNLIYYHSG
164

174 YVYGKYPNVRLDSLIEARLNLRMDETRMGVNRGSLGSPADMRNLINGIRNVRILHLS

183

1 match found in sequence:
US-09-708-427-25151 ; Sequence 25151, Application US/09708427
(from "/srch/paa/US097_COMB.pep")
Sequence 25151, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25151
LENGTH: 406
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..406
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc-feature
LOCATION: 1..406
OTHER INFORMATION: Ceres Seq. ID 1813390
Found using 'seq127c' (09-883727.key)

107 DLHVSVDGIGSDNVPDFTNRSVSKTFKRLKLCIDYDQNPDTVSFDPPNLYLEYSD
157

167 YVAVKYPVRKFCSLVEASLNLQMTYDCAQASYGFLVGNATDFLMGVSNVQILHLSDKSL
176

1 match found in sequence:
US-09-708-427-25152 ; Sequence 25152, Application US/09708427
(from "/srch/paa/US097_COMB.pep")
Sequence 25152, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25152
LENGTH: 388
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..388
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc-feature
LOCATION: 1..388
OTHER INFORMATION: Ceres Seq. ID 1813391
Found using 'seq127c' (09-883727.key)

89 DLHVSVDRGIGSDNVYEDFTNRSVSSKTFKRLKLCIDYDQNPDTVSFDIPNLVLEYEYSD
139

149 YVAVKYPRVFCSLVEASLNLQMTYDOCAQASVGLVGNATDPLMGVSNVOILHLSKSL
158

1 match found in sequence:

US-09-708-427-25153 ; Sequence 25153, Application US/09708427

(from "/src/h/paa/US097-COMB.pep")

Sequence 25153, Application US/09708427

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85366

SOFTWARE: PatentIn version 3.1

SEQ ID NO 25153

LENGTH: 377

TYPE: PRT

ORGANISM: Arabidopsis thaliana

FEATURE:

NAME/KEY: misc.feature

LOCATION: 1..377

OTHER INFORMATION: Xaa is any amino acid

LOCATION: 1..377

OTHER INFORMATION: Ceres Seq. ID 1813392

Found using 'seq127c' (09-883727.key)

78 DLHVSVDRGIGSDNVYEDFTNRSVSSKTFKRLKLCIDYDQNPDTVSFDIPNLVLEYEYSD
128

138 YVAVKYPRVFCSLVEASLNLQMTYDOCAQASVGLVGNATDPLMGVSNVOILHLSKSL
147

1 match found in sequence:

US-09-791-537-68226 ; Sequence 68226, Application US/09791537

(from "/src/h/paa/US097-COMB.pep")

Sequence 68226, Application US/09791537

GENERAL INFORMATION:

APPLICANT: Biomimix, Inc.

APPLICANT: Debe, Derek

APPLICANT: Danzer, Joseph

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: PatentIn version 3.0

SEQ ID NO 68226

LENGTH: 321

TYPE: PRT

ORGANISM: Caenorhabditis elegans

Found using 'seq127c' (09-883727.key)

33 TVQVSIKAVREILIEBANQVIDTPYICGDIHGQFHDLMELFRVGSPPNTNVLFGD
83

93 YVDRGNVSVEFFILLMLLKCRYPDRITLLIRGNHESROIQVYGYFDECVRKRYGSGQWAKH
102

1 match found in sequence:

US-09-791-537-118672 ; Sequence 118672, Application US/09791537

(from "/src/h/paa/US097-COMB.pep")

Sequence 118672, Application US/09791537

GENERAL INFORMATION:

APPLICANT: Biomimix, Inc.

APPLICANT: Debe, Derek

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEM

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: PatentIn version 3.0

SEQ ID NO 118672

LENGTH: 713

TYPE: PRT

ORGANISM: Caenorhabditis elegans

Found using 'seq127c' (09-883727.key)

24 KTQTLQNRQTMVHLEFKKADVAKECENFLQYGYGAVQVSPWEHLKAFPNNNYPMWVR
74

84 YQPVSYKLDSSRGNEQFQDMVNRCKVGRILIVDVMNHWGIGQKSGNGCVSSGSSSF
93

1 match found in sequence:

US-09-791-537-147748 ; Sequence 147748, Application US/09791537

(from "/src/h/paa/US097-COMB.pep")

Sequence 147748, Application US/09791537

GENERAL INFORMATION:

APPLICANT: Biomimix, Inc.

APPLICANT: Debe, Derek

APPLICANT: Danzer, Joseph

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEM

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: PatentIn version 3.0

SEQ ID NO 147748

LENGTH: 784

TYPE: PRT

ORGANISM: Arabidopsis thaliana

Found using 'seq127c' (09-883727.key)

131 FWTIDLEKHVGDTWEIITHIPKNSLDVCLTKGTSTPIISVLRLSLPNNTYITRESG
181

191 YPDDEYDRKWVYFESEMRQISTILKVNNTINGFLAQEVLMTAAPSASVPLSFTKDL

200

1 match found in sequence:
US-09-883-727A-127 : Sequence 127, Application US/09883727A
(from "/srch/paa/us098_COMB.pep")
Sequence 127, Application US/09883727A
GENERAL INFORMATION:
APPLICANT: West, Robert R.
APPLICANT: Sheppard, Paul O.
APPLICANT: Fox, Brian
TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of
FILE REFERENCE: 00-33
CURRENT APPLICATION NUMBER: US/09/883,727A
CURRENT FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 127
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: VARIANT
LOCATION: (3)...(3)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: VARIANT
LOCATION: (4)...(4)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: MUTAGEN
LOCATION: (6)...(6)
OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
NAME/KEY: MUTAGEN
LOCATION: (7)...(7)
OTHER INFORMATION: Xaa = sulfated tyrosine
NAME/KEY: MUTAGEN
LOCATION: (8)...(8)
OTHER INFORMATION: Xaa = 2-sulfotyrosine
NAME/KEY: VARIANT
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: VARIANT
LOCATION: (10)...(10)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: MUTAGEN
LOCATION: (12)...(12)
OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
NAME/KEY: MUTAGEN
LOCATION: (13)...(13)
OTHER INFORMATION: Xaa = sulfated tyrosine
NAME/KEY: MUTAGEN
LOCATION: (14)...(14)
OTHER INFORMATION: Xaa = 2-sulfotyrosine
NAME/KEY: VARIANT
LOCATION: (15)...(15)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: MUTAGEN
LOCATION: (17)...(17)
OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
NAME/KEY: MUTAGEN
LOCATION: (18)...(18)
OTHER INFORMATION: Xaa = sulfated tyrosine
NAME/KEY: MUTAGEN
LOCATION: (19)...(19)
OTHER INFORMATION: Xaa = 2-sulfotyrosine
NAME/KEY: VARIANT
LOCATION: (20)...(20)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: VARIANT
LOCATION: (21)...(21)

OTHER INFORMATION: Xaa = D or E, or is absent
Found using 'seq127c' (09-883727.key)

1

1
PNXXXXXXXXXXXXXXXXXX
20

1 match found in sequence:
US-09-883-727A-129 : Sequence 129, Application US/09883727A
(from "/srch/paa/us098_COMB.pep")
Sequence 129, Application US/09883727A
GENERAL INFORMATION:
APPLICANT: West, Robert R.
APPLICANT: Sheppard, Paul O.
APPLICANT: Fox, Brian
TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of
FILE REFERENCE: 00-33
CURRENT APPLICATION NUMBER: US/09/883,727A
CURRENT FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 129
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Formula of a complement C1s Inhibitor
LOCATION: (3)...(3)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: VARIANT
LOCATION: (4)...(4)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: MUTAGEN
LOCATION: (6)...(6)
OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
NAME/KEY: MUTAGEN
LOCATION: (7)...(7)
OTHER INFORMATION: Xaa = sulfated tyrosine
NAME/KEY: MUTAGEN
LOCATION: (8)...(8)
OTHER INFORMATION: Xaa = 2-sulfotyrosine
NAME/KEY: VARIANT
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: VARIANT
LOCATION: (10)...(10)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: MUTAGEN
LOCATION: (12)...(12)
OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
NAME/KEY: MUTAGEN
LOCATION: (13)...(13)
OTHER INFORMATION: Xaa = sulfated tyrosine
NAME/KEY: MUTAGEN
LOCATION: (14)...(14)
OTHER INFORMATION: Xaa = 2-sulfotyrosine
NAME/KEY: VARIANT
LOCATION: (15)...(15)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: MUTAGEN
LOCATION: (17)...(17)
OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
NAME/KEY: MUTAGEN
LOCATION: (18)...(18)
OTHER INFORMATION: Xaa = sulfated tyrosine
NAME/KEY: MUTAGEN
LOCATION: (19)...(19)
OTHER INFORMATION: Xaa = 2-sulfotyrosine
NAME/KEY: VARIANT
LOCATION: (20)...(20)

OTHER INFORMATION: Xaa = D or E
Found using 'seq127c' (09-883727.key)

1
1 PNXVXXXXXXXXXXXXXX
20

1 match found in sequence:

US-09-935-625-16712 : Sequence 16712, Application US/09935625

(from "/src/h/paa/US099_COMB.pep")

Sequence 16712, Application US/09935625

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE

TITLE OF INVENTION: MODULATING VARIOUS RESPONSES

FILE REFERENCE: 2750-1481P

CURRENT APPLICATION NUMBER: US/09/935,625

CURRENT FILING DATE: 2001-08-24

NUMBER OF SEQ ID NOS: 33136

SEQ ID NO 16712

LENGTH: 193

TYPE: PRT

ORGANISM: Arabidopsis thaliana

FEATURE:

NAME/KEY: peptide

LOCATION: 1..193

OTHER INFORMATION: Ceres Seq. ID no. 2113886

Found using 'seq127c' (09-883727.key)

1 MPTTSSPTLRLSLVHYEHFESVISPDLPNLELYDSYDALYGPVQVNEISLVEAYLNT
30

61 DKAEHVESPDVTKLIMGIRNVEILSLSPDSVGVYISCK 49

1 match found in sequence:

US-09-935-625-16875 : Sequence 16875, Application US/09935625

(from "/src/h/paa/US099_COMB.pep")

Sequence 16875, Application US/09935625

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE

TITLE OF INVENTION: MODULATING VARIOUS RESPONSES

FILE REFERENCE: 2750-1481P

CURRENT APPLICATION NUMBER: US/09/935,625

CURRENT FILING DATE: 2001-08-24

NUMBER OF SEQ ID NOS: 33136

SEQ ID NO 16875

LENGTH: 497

TYPE: PRT

ORGANISM: Arabidopsis thaliana

FEATURE:

NAME/KEY: peptide

LOCATION: 1..497

OTHER INFORMATION: Ceres Seq. ID no. 2172264

Found using 'seq127c' (09-883727.key)

190 NVLAGCPVVEALYLNONGESMPTTSSPTLRLSLVHYEHFESVISPDLPNLELYDS
240

250 YALYGPVQVNEISLVEAYLNTDKAEHVESPDVTKLIMGIRNVEILSLSPDSVGVYISCK
259

1 match found in sequence:

US-09-935-625-16876 : Sequence 16876, Application US/09935625

(from "/src/h/paa/US099_COMB.pep")

Sequence 16876, Application US/09935625

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE

TITLE OF INVENTION: MODULATING VARIOUS RESPONSES

FILE REFERENCE: 2750-1481P

CURRENT APPLICATION NUMBER: US/09/935,625

CURRENT FILING DATE: 2001-08-24

NUMBER OF SEQ ID NOS: 33136

SEQ ID NO 16876

LENGTH: 435

TYPE: PRT

ORGANISM: Arabidopsis thaliana

FEATURE:

NAME/KEY: peptide

LOCATION: 1..435

OTHER INFORMATION: Ceres Seq. ID no. 2172265

Found using 'seq127c' (09-883727.key)

128 NVLAGCPVVEALYLNONGESMPTTSSPTLRLSLVHYEHFESVISPDLPNLELYDS
178

188 YALYGPVQVNEISLVEAYLNTDKAEHVESPDVTKLIMGIRNVEILSLSPDSVGVYISCK
197

1 match found in sequence:

US-09-935-625-16877 : Sequence 16877, Application US/09935625

(from "/src/h/paa/US099_COMB.pep")

Sequence 16877, Application US/09935625

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE

TITLE OF INVENTION: MODULATING VARIOUS RESPONSES

FILE REFERENCE: 2750-1481P

CURRENT APPLICATION NUMBER: US/09/935,625

CURRENT FILING DATE: 2001-08-24

NUMBER OF SEQ ID NOS: 33136

SEQ ID NO 16877

LENGTH: 287

TYPE: PRT

ORGANISM: Arabidopsis thaliana

FEATURE:

NAME/KEY: peptide

LOCATION: 1..287

OTHER INFORMATION: Ceres Seq. ID no. 2172266

Found using 'seq127c' (09-883727.key)

1 MPTTSSPTLRLSLVHYEHFESVISPDLPNLELYDSYDALYGPVQVNEISLVEAYLNT
30

61 DKAEHVESPDVTKLIMGIRNVEILSLSPDSVGVYISCK 49

1 match found in sequence:

US-60-360-039-5904 : Sequence 5904, Application US/60360039

(from "/src/h/paa/US60_COMB.pep")

Sequence 5904, Application US/60360039

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5904
LENGTH: 321
TYPE: PRT
ORGANISM: Caenorhabditis elegans
Found using 'seq127c' (09-883727.key)

33 TQVSKAKREILIEANVOIDTPTICGDHGFHDLMELEFRVGGSPNTNIFLGD
-----|-----
63

93 YVDRGVNSVEFFILMLKCRYPDRITLIRGNHESRQITQVYGFYDECVRKYGSGQVWKH
-----|-----
102

1 match found in sequence:
US-60-360-039-6558 ; Sequence 6558, Application US/60360039
(from "/srch/paa/US60.COMB.pep")
Sequence 6558, Application US/60360039
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 6558
LENGTH: 713
TYPE: PRT
ORGANISM: Caenorhabditis elegans
Found using 'seq127c' (09-883727.key)

24 KTQTLQRQTMVHLEWKMADVAKECENFLQYGYGAVOVSPMEHLKAFPNNNYPMWVR
-----|-----
74

84 YQPVSYLDRSGNDEFDQMVNRCNKVGVRIIVDMNHMVIGIGKSGNGVGSSGSSSF
-----|-----
93

1 match found in sequence:
US-60-382-898-13 ; Sequence 13, Application US/60382898
(from "/srch/paa/US60.COMB.pep")
Sequence 13, Application US/60382898
GENERAL INFORMATION:
APPLICANT: Hudson, Keith
APPLICANT: et al.
TITLE OF INVENTION: Plant Receptors and Ligands
FILE REFERENCE: 1066P

CURRENT APPLICATION NUMBER: US/60/382,898
CURRENT FILING DATE: 2002-05-22
NUMBER OF SEQ ID NOS: 1344
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 784
TYPE: PRT
ORGANISM: Arabidopsis thaliana
Found using 'seq127c' (09-883727.key)

131 FWTIDLEKHVGDTEWELIHIKPSNSLDVCLITGTSTPIISVLELRSPNNNTYITEG
-----|-----
181

191 YPDDFYRKWVPYFESFMRQISTILKVNNTINGFLAPQEVMTAAPSMSVPLSTKDL
-----|-----
200

1 match found in sequence:
US-09-950-084-4809 ; Sequence 4809, Application US/09950084
(from "/srch/paa/US09_NMW.COMB.pep")
Sequence 4809, Application US/09950084
GENERAL INFORMATION:
APPLICANT: George H. Shimer, Jr.
APPLICANT: George H. Miller
APPLICANT: Roberta S. Hare
APPLICANT: Karen J. Shaw
TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
FILE REFERENCE: 1034/IC9630S2
CURRENT APPLICATION NUMBER: US/09/950,084
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: US 09/417,811
PRIOR FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: US 09/353,718
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 09/266,557
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,556
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,555
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,542
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,541
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/037,934
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: US 09/036,720
PRIOR FILING DATE: 1998-03-06
PRIOR APPLICATION NUMBER: US 09/036,338
PRIOR FILING DATE: 1998-03-06
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 7451
SEQ ID NO 4809
LENGTH: 313
TYPE: PRT
ORGANISM: Staphylococcus aureus
Found using 'seq127c' (09-883727.key)

215 ISSHHHHHGKSMYTFGTGIDRQLFYQFMKLRESVLRLKGYVSRNPNATYEBOYA
-----|-----
265

275 YGLPDYGLIGMOLPLTIVIGELDTNHIRNQLDLOFT
-----|-----
284

1 match found in sequence:

US-10-282-122A-45985 ; Sequence 45985, Application US/10282122A
(from "/src/h/paa/US10_NEW_COMB.pep")
Sequence 45985, Application US/10282122A

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16

Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1
SEQ ID NO 45985

LENGTH: 284

TYPE: PRT

ORGANISM: Bacillus anthracis

FEATURE:

NAME/KEY: MISC_FEATURE

LOCATION: (185) ..(185)

OTHER INFORMATION: X-any amino acid

FEATURE:

NAME/KEY: MISC_FEATURE

LOCATION: (226) ..(226)

OTHER INFORMATION: X-any amino acid

Found using 'seq127c' (09-883727.key)

199

SNFRGIRPLKRNHTGNGKITLPRMPXEHFIFODEYKRAMDFIYGMLENSGKPRDS

259

YPFEYRNDPKQHPKHKHIVDIYVPI

268

1 match found in sequence:

US-10-282-122A-46109 ; Sequence 46109, Application US/10282122A

(from "/src/h/paa/US10_NEW_COMB.pep")
Sequence 46109, Application US/10282122A
GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16

Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1
SEQ ID NO 46109

LENGTH: 296

TYPE: PRT

ORGANISM: Bacillus anthracis

Found using 'seq127c' (09-883727.key)

208

LCITIPGESATETNDIGIMVIPSGKYAVGHFIFODEYKRAMDFIYGMLENSGKPRDS

258

YPFEYRNDPKQHPKHKHIVDIYVPIEPF

277

1 match found in sequence:

US-10-369-493-5904 ; Sequence 5904, Application US/10369493
(from "/src/h/paa/US10_NEW_COMB.pep")
Sequence 5904, Application US/10369493

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5904
LENGTH: 321
TYPE: PRT
ORGANISM: Caenorhabditis elegans
Found using 'seq127c' (09-883727.key)

33 TQVKSICAKVREILIEBANQVIDPTVTCIGDIGHQFHDIMLEFRVGGSPPTNYLFLGD
83

93 YVDRGYNSTVEFLLMLMKCRYPDRITLLINGNHESRQITQVYGFYDECVARKYSGQYWKH
102

1 match found in sequence:
US-10-369-493-6558; Sequence 6558, Application US/10369493
(from "/sich/paa/US10_NEW_COMB.pep")
Sequence 6558, Application US/10369493
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 6558
LENGTH: 713
TYPE: PRT
ORGANISM: Caenorhabditis elegans
Found using 'seq127c' (09-883727.key)

24 KTOTLONRQTMVHLEFKMKADVAKECENFLQYGYGAVOVSPMEHLKAFNNNYPWVR
74

84 YQPVSYKLDISRGNEQFQDMVNRCKNVGRIIVDVMNMHVGIGQKSGNGVSSSSSF
93

-- Search Statistics --
Times: CPU Total Elapsed
00:24:35.15 00:26:45.00
Number of sequences searched: 5594650
Number of sequence hits: 40
Number of separate matches: 40
Number of sequence hits saved: 0

1 FINDPATTERNS on pir:* allowing 0 mismatches
1 PNXXXXXXXXXXXXXXXXXX June 11, 2003 07:20 ...
1 T27049 ck: 8651 len: 321 i phosphoprotein phosphatase (EC 3.1.3.16) Y4
83: VGGSP PNTNPLFLGDYVDRGNSVE TFIIL
D71316 ck: 7074 len: 329 i conserved hypothetical protein TP0496 - SYF
146: RPAEV PNVSTVLGKAYIQRGYYAD LAVKY
T39918 ck: 185 len: 519 i probable acetyl-coenzyme a transporter - fi
79: PYFLK PNVSTSLATYSLAAYPSL KVLMS
B84702 ck: 1354 len: 421 i hypothetical protein At2g29910 [imported]
227: CMERT PNLVYLDSSYVPMYEVDL GSLVE
T48993 ck: 6038 len: 425 i hypothetical protein F25L23.110 - Arabidops
201: VLFDT PNLVYLRKSDYVAAKPKVN FSSLV
T18815 ck: 2724 len: 160 i hypothetical protein C01G10.4 - Caenorhabdi
112: TYYTY PNNYNNNNNGYTFYYYPNN NNGY
T45697 ck: 5021 len: 784 i hypothetical protein F18L15.120 - Arabidops
181: ELNSL PNNYITGESGPDDEFYDRKW VPYFE
E90460 ck: 2142 len: 545 i hypothetical protein SSO2830 [imported] - S
377: LSONN PNNYSLATOTYQLYLPGE SGFTY
D86201 ck: 9833 len: 2,025 i protein F12K11.6 [imported] - Arabidopsis t
654: ISFDL PNLLEYLDYSDALGYQVN LESLV
E84857 ck: 8550 len: 737 i hypothetical protein At2g42730 [imported] -
233: ISLDA PNLITYKHSGYVLGKYPNVK LDSLI
A84514 ck: 7461 len: 406 i hypothetical protein At2g14090 [imported] -
157: VSEFD PNLVYLEYSDYVAVKYPVK FCSLV
T41715 ck: 2217 len: 578 i hypothetical protein SPAC821.04c - fission
454: VPAIP PNVPTFEVDPTACYINN SYLPP
T20090 ck: 7848 len: 713 i hypothetical protein C50B6.7 - Caenorhabdit
74: HLKAF PNNYTPMWVRYQPVSIRLDS RSGNE
G84053 ck: 538 len: 302 i hybrid-endo-beta-1,3-1,4 glucanase BH3231
PNXXXXXXXXXXXXXXXXXXXX

7: ELISIR PNH5YAAPYNECAEYSTNH FYGYG
C75068 ck: 3829 len: 787 i probable beta-galactosidase (EC 3.2.1.23)
132: PNGSL PNDIYPPITLHPILYLEEV MKWYE
A97093 ck: 4977 len: 416 i probable membrane protein [imported] - C
237: SLNLD PNNFTDKNNINFTYKDAF AGSMA
H89839 ck: 8099 len: 308 i hypothetical protein SA0642 [imported] -
260: SFRNQ PNAITEFOYATGLPDYGITG MQLPL
Databases searched:
NBRF, Release 73.0, Released on 16Aug2002, Formatted on 20Aug2002
Total finds: 17
Total lengths: 96,134,422
Total sequences: 283,224
CPU time: 55.47


```
1 FINDPATTERNS on swp:* allowing 0 mismatches
1 1 PNXKXXXXXXXXXXXXXXXXX June 11, 2003 07:22 ...
1 BC83_ACEXY ck: 9549 len: 804 1 Q9w62 acetobacter xylinus. cyclic di-gmp b
1 544: HITRM PNLAYMASAGPFTTYADLS RSAYV PNXKXXXXXXXXXXXXXXXXX
1 Q9w62 ck: 9549 len: 804 1 Q9w62 acetobacter xylinus. bcsbi protein.
1 544: HITRM PNLAYMASAGPFTTYADLS RSAYV PNXKXXXXXXXXXXXXXXXXX
1 Q9USW4 ck: 185 len: 519 1 Q9usw4 schizosaccharomyces pombe (fission y
1 79: PYFLK PNVSTSLATYSLAAYPSL KVLMS PNXKXXXXXXXXXXXXXXXXX
1 Q9UT49 ck: 2217 len: 578 1 Q9ut49 schizosaccharomyces pombe (fission y
1 454: VPAIP PNVPTFVDPTTACTYNN SYLPP PNXKXXXXXXXXXXXXXXXXX
1 Q93164 ck: 2724 len: 160 1 Q93164 caenorhabditis elegans. colg10.4 pro
1 112: TYYY PNNVNNNGYTYYYYPN NNGY PNXKXXXXXXXXXXXXXXXXX
1 P91982 ck: 7848 len: 713 1 P91982 caenorhabditis elegans. c50b6.7 prot
1 74: HLKAF PNNYPWVRYPVSXKLS RSGNE PNXKXXXXXXXXXXXXXXXXX
1 Q9XT8 ck: 8851 len: 321 1 Q9xt8 caenorhabditis elegans. y49e10.3 pro
1 83: VGGSP PNTNYLFLGDYDRGINSVE TFLIL PNXKXXXXXXXXXXXXXXXXX
1 Q96603 ck: 9301 len: 321 1 Q966q3 caenorhabditis elegans. ser/thr prot
1 83: VGGSP PNTNYLFLGDYDRGINSVE TFLIL PNXKXXXXXXXXXXXXXXXXX
1 Q9GLN7 ck: 8920 len: 1,304 1 Q9gln7 pan troglodytes (chimpanzee). dipept
1 482: FSGRT PMSRYNEDMWYLRKYGIC PPVTR PNXKXXXXXXXXXXXXXXXXX
1 Q9LUK1 ck: 3748 len: 302 1 Q9luk1 arabidopsis thaliana (mouse-ear cres
1 171: LSIYT PNLVYLDYSDYLCVNSN HFNDL PNXKXXXXXXXXXXXXXXXXX
1 Q9SUI3 ck: 8550 len: 737 1 Q9sui3 arabidopsis thaliana (mouse-ear cres
1 233: ISLDA PNLIIYKHSGYLGKYPNVK LDSLI PNXKXXXXXXXXXXXXXXXXX
1 Q9SIK6 ck: 1354 len: 421 1 Q9sik6 arabidopsis thaliana (mouse-ear cres
1 227: CMFRT PNLVYLDYSSYVPMWEVDL GSLVE PNXKXXXXXXXXXXXXXXXXX
1 Q9SHK4 ck: 9833 len: 2,025 1 Q9shk4 arabidopsis thaliana (mouse-ear cres
1 654: ISFDL PNLVYLDYSDYLGYPQVN LESLV PNXKXXXXXXXXXXXXXXXXX
1 Q9LX46 ck: 6038 len: 425 1 Q9lx46 arabidopsis thaliana (mouse-ear cres
1 PNXKXXXXXXXXXXXXXXXXX

1 201: VLFDL PNLVYLYKSDYVAAKYPKN FSSLY
1 Q8S1S4 ck: 8679 len: 907 1 Q8s1s4 oryza sativa (japonica cultivar-g
1 196: SSSSL PNNSYHYHQYQNMPEYYDO SAPSS PNXKXXXXXXXXXXXXXXXXX
1 Q9IH62 ck: 9840 len: 602 1 Q9ih62 nipah virus. glycoprotein (attach
1 276: WTPPN PNTVYHCSAVYNNFEYYLC AVSTV PNXKXXXXXXXXXXXXXXXXX
1 083509 ck: 7074 len: 329 1 083509 treponema pallidum. hypothetical
1 146: RPAEV PNVSTVLRATYORGYVAD LAVKY PNXKXXXXXXXXXXXXXXXXX
1 Q9K7X6 ck: 538 len: 302 1 Q9k7x6 bacillus halodurans. hybrid-endo-
1 7: ELSTR PNHSTAAPYNECAEYSTNH FYGKG PNXKXXXXXXXXXXXXXXXXX
1 Q97IS5 ck: 4977 len: 416 1 Q97is5 clostridium acetobutylicum. predi
1 237: SLNLD PNNFYTDKNNTNFITYKDAF AGSMA PNXKXXXXXXXXXXXXXXXXX
1 Q99V74 ck: 8099 len: 308 1 Q99v74 staphylococcus aureus (strain mu5
1 260: SFRNQ PNAIFYEQAYGLPDYGHIG MQLPL PNXKXXXXXXXXXXXXXXXXX
1 Q8XM06 ck: 4156 len: 314 1 Q8xm06 clostridium perfringens. hypothet
1 158: SLICE PMSIYTRKNAVIVNVDLKL LEINS PNXKXXXXXXXXXXXXXXXXX
1 Q8RF83 ck: 9203 len: 539 1 Q8rf83 fusobacterium nucleatum (subsp. n
1 136: KIIEV PNYYNIFKNVYTDYKEYL KITSK PNXKXXXXXXXXXXXXXXXXX
1 Q9HJZ2 ck: 6354 len: 391 1 Q9hjz2 thermoplasma acidophilum. probabl
1 315: SKRIY PNTDYFSGIYVLAGYPLRN NIYTS PNXKXXXXXXXXXXXXXXXXX
1 Q97V07 ck: 2142 len: 545 1 Q97v07 sulfolobus solfataricus. hypothet
1 377: LSGNN PNNVYSLATQYOLQYLPGF SGFIY PNXKXXXXXXXXXXXXXXXXX
1 Q9UYH2 ck: 3829 len: 787 1 Q9uyh2 pyrococcus abyssi. beta-galactosi
1 132: PNGSL PNDIYYPRITYLPIYLEYV MKWYE PNXKXXXXXXXXXXXXXXXXX
1 Q8TMS3 ck: 2546 len: 1,051 1 Q8tms3 methanosarcina acetivorans. wd-do
1 412: KVFFS PNGKTYATMSYGSTAYVWNA SYREQ PNXKXXXXXXXXXXXXXXXXX

Databases searched:
SWISS-PROT, Release 40.3, Released on 9Aug2002, Formatted on 20Aug2002
SPTREMBL, Release 21.0, Released on 15Jun2002, Formatted on 28Jun2002

Total finds: 26
Total length: 247,523,443
Total sequences: 784,472
CPU time: 02:40.45
```


> 0 <
0110 Intelligenetics
> 0 <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "seq127c-wpat" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.

Selected sequence key from "09-883727.key":

seq127c (AA) ID seq127c AA preliminary pattern
followed by

1 pn
2 any character
2 any character
2 y
2 any character
2 any character
2 any character
2 any character
2 any character
2 y
2 any character
2 any character
2 any character
2 any character
2 y
2 any character
2 any character
2 any character
2 any character

Selected data banks and files:

Data bank : A-GenesSeq 35.2, all entries

-- Output Parameters --

Format Options:

Nucleic acid code matching	Exact	File Options:	
Find non-matching hits only	No	Indirect file	NO
Report key used	Yes	Sequence or key file	NO
Note position of hit	Yes	List of hits	NO
Display full annotations	Yes	Hit display	Yes
Sequence context	50	Name and annotations	Yes

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	No

No hits found.

-- Search Statistics --

Times:	CPU	Total Elapsed
	00:00:19.07	00:00:22.00
Number of sequences searched:		170751
Number of sequence hits:		0
Number of separate matches:		0
Number of sequence hits saved:		0

> 0 < Intelligenetics
> 0 <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "seq127c-iss" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.

Selected sequence key from "09-883727.key":

seq127c (AA) ID seq127c AA preliminary pattern
followed by

1 pn
2 any character
2 any character
2 y
2 any character
2 any character
2 any character
2 any character
2 any character
2 any character
2 y
2 any character
2 any character
2 any character
2 any character
2 any character
2 any character
2 any character
2 any character
2 any character
2 any character
2 any character

Selected data banks and files:

Data bank : Issued_AA , all entries

-- Output Parameters --

Format Options:		File Options:	
Nucleic acid code matching	Exact	Indirect file	NO
Find non-matching hits only	No	Sequence or key file	NO
Report key used	Yes	List of hits	NO
Note position of hit	Yes	Hit display	Yes
Display full annotations	Yes	Name and annotations	Yes
Sequence context	50		

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	NO

No hits found.

-- Search Statistics --

Times:	CPU	Total Elapsed
	00:01:18.08	00:01:22.00
Number of sequences searched:		262643
Number of sequence hits:		0
Number of separate matches:		0
Number of sequence hits saved:		0

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 11, 2003, 07:42:23 ; Search time 15 Seconds

(without alignments)
134.588 Million cell updates/sec

Title: US-09-883-727a-127

Perfect score: 50

Sequence: 1 PNMXXXXXXXXXXXXXXXXXX 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues 634

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 20

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	36.0	20	2	S67990
2	13	26.0	20	2	E60894
3	13	26.0	20	2	S06466
4	13	26.0	20	2	A47687
5	13	26.0	20	2	S39380
6	13	26.0	20	2	A61093
7	13	26.0	20	2	A60365
8	13	26.0	20	2	PH1341
9	13	26.0	20	2	S71593
10	13	26.0	20	2	PH1783
11	13	26.0	20	2	A47177
12	13	26.0	20	2	I40066
13	13	26.0	20	2	A60975
14	13	26.0	20	2	S08558
15	13	26.0	20	2	S09516
16	13	26.0	20	2	S05031
17	13	26.0	20	2	E41316
18	13	26.0	20	2	S03986
19	13	26.0	20	2	S03481
20	12	24.0	20	2	A37111
21	12	24.0	20	2	S03335
22	12	24.0	20	2	P00300
23	12	24.0	20	2	S53440
24	12	24.0	20	2	UC5589
25	12	24.0	20	2	A61276
26	12	24.0	20	2	S03954
27	12	24.0	20	2	I55270
28	12	24.0	20	2	I58423
29	11	22.0	20	2	B53875

30	11	22.0	20	2	G61491	seed protein ws-25
31	11	22.0	20	2	A49048	T-cell receptor be
32	11	22.0	20	2	PS0087	microbial serine p
33	11	22.0	20	2	S61281	probable L-histidi
34	11	22.0	20	2	A57106	hull allergen Gly
35	11	22.0	20	2	D49255	T-cell receptor be
36	11	22.0	20	2	S03508	T-cell receptor al
37	11	22.0	20	2	S44465	pyrrolicoridin - py
38	11	22.0	20	2	A61487	110K Atpase, lntes
39	11	22.0	20	2	S02643	RNA-directed RNA p
40	11	22.0	20	2	S49040	dps-protein 19K -
41	11	22.0	20	2	S01816	hemoglobin Biv - t
42	10	20.0	20	2	PN0133	pepsin (EC 3.4.23.
43	10	20.0	20	2	A05332	serum amyloid P-co
44	10	20.0	20	2	PL0161	hemagglutinin - In
45	10	20.0	20	2	PQ0046	citrate (sl)-synth
46	10	20.0	20	2	A47105	dystroglycan - chl
47	10	20.0	20	2	S37684	protein IEF SSP 91
48	10	20.0	20	2	A85659	hypothetical prote
49	10	20.0	20	2	PH1688	Ig heavy chain V r
50	10	20.0	20	2	PD0015	actin-binding prot
51	10	20.0	20	2	S28436	major outer membra
52	10	20.0	20	2	S33676	protein kinase - r
53	9	18.0	20	2	A36045	thrombospondin hom
54	9	18.0	20	2	A42934	heat shock protein
55	9	18.0	20	2	S65399	immunodeficiency v
56	9	18.0	20	2	A37988	acid proteinase be
57	9	18.0	20	2	I67551	monocyte chemotact
58	9	18.0	20	2	A60801	acrosome stabiliz
59	9	18.0	20	2	S38739	lipid transfer pro
60	9	18.0	20	2	S47202	T-cell receptor J-
61	9	18.0	20	2	PH1690	Ig heavy chain V r
62	9	18.0	20	2	PT0027	Ig heavy chain CDR
63	9	18.0	20	2	S78416	ribosomal protein
64	8	16.0	20	2	A60822	cytochrome P450 PB
65	8	16.0	20	2	S21176	testosterone 6beta
66	8	16.0	20	2	A60728	cytochrome P450 3A
67	8	16.0	20	2	PN1374	ferredoxin [2Fe-2S
68	8	16.0	20	2	PN0115	insulin-like growt
69	8	16.0	20	2	B44907	manganese peroxida
70	8	16.0	20	2	S63602	glutathione S-tran
71	8	16.0	20	2	S09022	carboxylesterase (
72	8	16.0	20	2	S09023	carboxylesterase (
73	8	16.0	20	2	S09023	acetylaminocyl-pept
74	8	16.0	20	2	S36842	chymotrypsin I (EC
75	8	16.0	20	2	A56900	venombin B (EC 3.4
76	8	16.0	20	2	PX0042	fructose-bisphosph
77	8	16.0	20	2	A20999	15K protein B - ra
78	8	16.0	20	2	B38382	GFP-binding protei
79	8	16.0	20	2	A38566	chromogranin-B - r
80	8	16.0	20	2	C49164	chromogranin-B - r
81	8	16.0	20	2	D49164	chromogranin-B - r
82	8	16.0	20	2	A49164	chromogranin-B - r
83	8	16.0	20	2	A45806	T-cell receptor be
84	8	16.0	20	2	B33761	actin - Acanthamo
85	8	16.0	20	2	A39543	collagen alpha 1(I
86	8	16.0	20	2	S08605	hypothetical prote
87	8	16.0	20	2	B45174	RNA-binding protei
88	8	16.0	20	2	S33001	hypothetical prote
89	8	16.0	20	2	T44453	acetyl-CoA synthet
90	8	16.0	20	2	B44920	2-haloaczoate 1,2
91	8	16.0	20	2	A44927	major outer membra
92	8	16.0	20	2	S33867	guinaldic acid 4-o
93	8	16.0	20	2	T48881	leader peptide [Im
94	8	16.0	20	2	S63490	disulfide isomerase
95	8	16.0	20	2	B39089	hydrogenase (EC 1.
96	8	16.0	20	2	PA0022	protein QA10011 -
97	8	16.0	20	2	A60150	inulinase (EC 3.2.
98	8	16.0	20	2	PC2084	serine proteinase
99	8	16.0	20	2	PC1152	equilatorin 1D
100	8	16.0	20	2	S68785	cathepsin L (EC 3.
101	8	16.0	20	2	A60295	apolipoprotein III
102	8	16.0	20	2	A49142	hyaluronidase (EC

103	8	16.0	20	2	S77989	cytochrome-c oxida
104	8	16.0	20	2	S77992	cytochrome-c oxida
105	8	16.0	20	2	A34859	heathermine - Mex
106	8	16.0	20	2	S46479	retinoid-X-recepto
107	8	16.0	20	2	S28405	lamin B receptor -
108	8	16.0	20	2	TS4189	galactose-1-phosph
109	8	16.0	20	2	PH1326	Ig heavy chain DJ
110	8	16.0	20	2	S27350	lysophospholipase
111	8	16.0	20	2	P00033	aldose 1-epimerase
112	8	16.0	20	2	P00071	T-cell receptor be
113	8	16.0	20	2	P00537	arylhydroxamic aci
114	8	16.0	20	2	A60897	class I histocompa
115	8	16.0	20	2	A31516	lectin, galactose/
116	8	16.0	20	2	S11416	ribosomal protein
117	8	16.0	21	2	PX0078	alanine dehydrogen
118	8	16.0	21	2	PT0089	4-hydroxybenzoate
119	8	16.0	21	2	S18549	dihydrolipoamide S
120	8	16.0	21	2	TS4351	gene HEXA protein
121	8	16.0	21	2	S69371	duodenase - bovine
122	8	16.0	21	2	A35646	mast cell proteina
123	8	16.0	21	2	IS1224	somatotropin - chi
124	8	16.0	21	2	D38837	T-cell receptor be
125	8	16.0	21	2	PN0082	sperm chromatin pr
126	8	16.0	21	2	A02903	alpha-crystallin c
127	8	16.0	21	2	S69502	NI/CAR-binding t
128	8	16.0	21	2	A60696	nephritogenoside -
129	8	16.0	21	2	G64564	hypothetical prote
130	8	16.0	21	2	H71858	hypothetical prote
131	8	16.0	21	2	JU0386	nitrile hydratase
132	8	16.0	21	2	S33688	guinaldic acid 4-o
133	8	16.0	21	2	A60684	L-ascorbate peroxi
134	8	16.0	21	2	F28027	protein p9 - curle
135	8	16.0	21	2	PQ0145	glucan endo-1,3-be
136	8	16.0	21	2	S27247	pseudogerm - whe
137	8	16.0	21	2	S31427	biliary glycoprote
138	8	16.0	21	2	E41299	T-cell receptor al
139	8	16.0	21	2	S47207	T-cell receptor J-
140	8	16.0	21	2	PQ0789	NADH2 dehydrogenas
141	7	14.0	20	2	S29817	cytochrome P450 2C
142	7	14.0	20	2	A26380	cytochrome P450 4A
143	7	14.0	20	2	S04961	malate dehydrogena
144	7	14.0	20	2	S04958	malate dehydrogena
145	7	14.0	20	2	B61080	5-carboxymethyl-2-
146	7	14.0	20	2	S77981	cytochrome-c oxida
147	7	14.0	20	2	C44907	manganese peroxida
148	7	14.0	20	2	A54083	P190/210, fatty ac
149	7	14.0	20	2	B37520	glutathione transf
150	7	14.0	20	2	S29100	glutathione transf

ALIGNMENTS

RESULT 1
S67990
neurotoxin-associated protein type A Hm+ 17K chain - Clostridium botulinum (fragment)
N:Alternate names: HA-15 protein
C:Species: Clostridium botulinum
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 12-Jun-1998
C:Accession: S67990; C44644
R:Fujita, R.; Fujinaga, Y.; Inoue, K.; Nakajima, H.; Kunon, H.; Oguma, K.
FEBS Lett. 376, 41-44, 1995
A:Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin components
A:Reference number: S67988; MUID:96096783; PMID:8521962
A:Accession: S67990
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <PN>
R:Somers, E.; Dasgupta, B.R.
J. Protein Chem. 10, 415-425, 1991
A:Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without he
A:Reference number: A44644; MUID:92143938; PMID:1781887
A:Contents: type A

A:Accession: C44644
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <SOM>
A>Note: sequence extracted from NCBI backbone (NCBIP:83795)
C:Keywords: hemagglutinin

Query Match
Best Local Similarity 36.0%; Score 18; DB 2; Length 20;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
DB 8 PNGMV 12

RESULT 2
E60894
crystallin - Pacific cuttlefish (fragment)
C:Species: Sepia esculenta (Pacific cuttlefish)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jun-1994
C:Accession: E60894
R:Chou, S.H.
J. Protein Chem. 7, 527-534, 1988
A:Title: The protein sequence homology of gamma-crystallins among major vertebrate cl
A:Reference number: A60894; MUID:89351593; PMID:3255376
A:Accession: E60894
A:Molecule type: protein
A:Residues: 1-20 <CHR>
C:Superfamily: glutathione transferase
C:Keywords: eye lens

Query Match
Best Local Similarity 26.0%; Score 13; DB 2; Length 20;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
DB 1 PN 2

RESULT 3
S06466
T-cell receptor alpha chain J segment (DO) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 06-Jun-1997
C:Accession: S06466
R:Yague, J.; Blackman, M.; Born, W.; Marrack, P.; Kappler, J.; Palmer, E.
Nucleic Acids Res. 16, 11355-11364, 1988
A:Title: The structure of V-alpha and J-alpha segments in the mouse.
A:Reference number: S06466; MUID:89083566; PMID:2849763
A:Accession: S06466
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-20 <YAG>
A:Experimental source: strain Balb/c
C:Genetics:
A:Map position: 14
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein; heterodimer; T-cell receptor
F:1-18/Domain: J segment <JSE>
F:19-20/Domain: C region (fragment) <CRE>

Query Match
Best Local Similarity 26.0%; Score 13; DB 2; Length 20;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
DB 1 PN 2

RESULT 4

A47687
 3-dehydroquinate dehydratase (EC 4.2.1.10) - Amycolatopsis methanolica (fragment)
 C:Species: Amycolatopsis methanolica
 C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
 C:Accession: A47687
 R:Everink, G.J.; Hessels, G.I.; Vrijsloot, J.W.; Coggins, J.R.; Dijkhuizen, L.
 J. Gen. Microbiol. 138, 2449-2457, 1992
 A:Title: Purification and characterization of a dual function 3-dehydroquinate dehydratase
 A:Reference number: A47687; MUID:93123995; PMID:1479361
 A:Accession: A47687
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <EUV>
 A:Experimental source: WV2
 A:Note: Sequence extracted from NCBI backbone (NCBIP:122129)
 C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 26.0%; Score 13; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 ||
 Db 9 PN 10

RESULT 5
 S39380
 pectinesterase (EC 3.1.1.11) - papaya
 N:Alternate names: pectin methyl-esterase
 C:Species: Carica papaya (papaya)
 C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 17-Mar-1999
 C:Accession: S39380
 R:Lim, Y.M.; Chung, M.C.M.
 Arch. Biochem. Biophys. 307, 15-20, 1993
 A:Title: Isolation and characterization of pectin methyl-esterase from papaya.
 A:Reference number: S39380; MUID:94058247; PMID:8239653
 A:Accession: S39380
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <LIM>
 C:Keywords: carboxylic ester hydrolase

Query Match 26.0%; Score 13; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 ||
 Db 5 PN 6

RESULT 6
 A61093
 glue protein - California mussel (fragments)
 N:Alternate names: adhesive polypheolic protein
 C:Species: Mytilus californianus (California mussel)
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
 C:Accession: A61093
 R:Walte, J.H.
 J. Comp. Physiol. B 156, 491-496, 1986
 A:Title: Mussel glue from Mytilus californianus Conrad: a comparative study.
 A:Reference number: A61093; MUID:86279063; PMID:3734192
 A:Accession: A61093
 A:Molecule type: protein
 A:Residues: 1-20 <MAI>
 A:Note: the amino terminal residue was tentatively identified as Ser
 A:Note: 12-Ser was also found
 C:Comment: This glue protein is a component of the adhesive plaque of the byssus, the fi

C:Keywords: hydroxyproline; tandem repeat
 F:4,14/Modified site: 3-hydroxyproline (Pro) #status experimental
 F:5,9,15,19/Modified site: 4-hydroxyproline (Pro) #status experimental

F:7,17/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental
 F:13/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) (partial) #status experimental

Query Match 26.0%; Score 13; DB 2; Length 20;
 Best Local Similarity 40.0%; Pred. No. 4.1e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 PNXXY 5
 | |
 Db 9 PKITV 13

RESULT 7
 A60365
 trypsin inhibitor - tobacco hornworm (fragment)
 C:Species: Manduca sexta (tobacco hornworm)
 C>Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 03-Feb-1994
 C:Accession: A60365
 R:Kanoost, M.R.
 Insect Biochem. 20, 141-147, 1990
 A:Title: Isolation and characterization of four serine proteinase inhibitors (serpins
 A:Reference number: A60365
 A:Accession: A60365
 A:Molecule type: protein
 A:Residues: 1-20 <KAN>
 C:Keywords: hemolymph; monomer; serine proteinase inhibitor

Query Match 26.0%; Score 13; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 ||
 Db 6 PN 7

RESULT 8
 PH1341
 Ig heavy chain DJ region (clone C252-123) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PH1341
 R:Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A:Title: Predominance of fetal type DJH joining in young children with B precursor B1
 A:Reference number: PH1302; MUID:93094761; PMID:1460419
 A:Accession: PH1341
 A:Molecule type: DNA
 A:Residues: 1-20 <MAS>
 C:Keywords: heterotrimer; immunoglobulin

Query Match 26.0%; Score 13; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 ||
 Db 13 PN 14

RESULT 9
 S71593
 serine proteinase inhibitor, 33k - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 13-Sep-1998
 C:Accession: S71593
 R:Rao, C.N.; Liu, Y.Y.; Peavey, C.L.; Woodley, D.T.
 Arch. Biochem. Biophys. 317, 311-314, 1995
 A:Title: Novel extracellular matrix-associated serine proteinase inhibitors from huma
 A:Reference number: S71592; MUID:95177668; PMID:7672799
 A:Accession: S71593
 A:Molecule type: protein
 A:Residues: 1-20 <RAO>

C:Function:
A:Description: involved in turnover of connective tissues
C:Keywords: serine proteinase inhibitor

Query Match
Best Local Similarity 26.0%; Score 13; DB 2; Length 20;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
||
Db 6 PN 7

RESULT 10

PH1783
T cell receptor alpha chain V region (clone 2DN V alpha 24-4) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1783
R:Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; MUID:93301585; PMID:8391057
A:Accession: PH1783
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-20 <PQR>

Query Match
Best Local Similarity 26.0%; Score 13; DB 2; Length 20;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
||
Db 7 PN 8

RESULT 11

A41717
P100 protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 23-Mar-1993
C:Accession: A41717
R:Traub, L.M.; Segl-Eisenberg, R.
J. Biol. Chem. 266, 24642-24649, 1991
A:Title: Purification of p100, a protein antigenically related to the signal transducing
A:Reference number: A41717; MUID:92105130; PMID:1722209
A:Accession: A41717
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <TRA>

Query Match
Best Local Similarity 26.0%; Score 13; DB 2; Length 20;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
||
Db 16 PN 17

RESULT 12

I40066
shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)
C:Species: Buchnera aphidicola
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 11-Jun-1999
C:Accession: I40066
R:Roubakhs, D.; Baumann, P.
Gene 155, 107-112, 1995
A:Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (endos

A:Reference number: I40061; MUID:95212914; PMID:7535281
A:Accession: I40066

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-21 <RES>
A:Cross-references: EMBL:U10500; NID:9854719; PIDN:AAA79129.1; PID:9854720
C:Genetics:
A:Gene: arde
C:Superfamily: shikimate dehydrogenase; shikimate dehydrogenase homology
C:Keywords: oxidoreductase

Query Match
Best Local Similarity 26.0%; Score 13; DB 2; Length 21;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
||
Db 10 PN 11

RESULT 13

A60975
HMG1/2 homolog - axolotl (fragment)
C:Species: Ambystoma mexicanum (axolotl)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
C:Accession: A60975
R:Guillet, F.; Tournetier, A.; Denoulet, P.; Capony, J.P.; Kerfourn, F.; Charlemagne, Biol. Cell 69, 153-160, 1990
A:Title: High levels of HMG1-2 protein expression in the cytoplasm and nucleus of hyd
A:Reference number: A60975; MUID:91265891; PMID:2097001
A:Accession: A60975
A:Molecule type: protein
A:Residues: 1-21 <GVG>
A:Note: this protein was found in the cytoplasmic and nuclear compartments of thymocy
F:5-21/Domain: HMG box homology (fragment) <HMG>

Query Match
Best Local Similarity 26.0%; Score 13; DB 2; Length 21;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
||
Db 5 PN 6

RESULT 14

S08558
ribosomal protein L21 [validated] - Halobacterium salinarum (fragment)
N:Alternate names: ribosomal protein HL30
C:Species: Halobacterium salinarum
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jul-2000
C:Accession: S08558
R:Matheson, A.T.; Yaguchi, M.; Christensen, P.; Rollin, C.F.; Hasnain, S. Can. J. Biochem. Cell Biol. 62, 426-433, 1984
A:Title: Purification, properties, and N-terminal amino acid sequence of certain 50S
A:Reference number: S07437; MUID:84282108; PMID:6467081
A:Accession: S08558
A:Molecule type: protein
A:Residues: 1-21 <MAT>
A:Note: the source is designated as Halobacterium cutirubrum
A:Note: the protein is designated as ribosomal protein L30
C:Superfamily: Halocaula ribosomal protein HL31
C:Keywords: protein biosynthesis; ribosome

Query Match
Best Local Similarity 26.0%; Score 13; DB 2; Length 21;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
||
Db 1 PN 2

RESULT 15

S09516
 Protilamin - gama grass (fragment)
 C:Species: Tripsacum dactyloides (gama grass)
 C:Date: 21-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 09-May-1997
 C:Accession: S09516
 R:Biets, J.A.
 Biochem. Genet. 20, 1039-1053, 1982
 A:Title: Cereals protilamin evolution and homology revealed by sequence analysis.
 A:Reference number: S09165; MUID:83153005; PMID:7165690
 A:Accession: S09516
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-21 <BIE>
 C:Superfamily: zeln

Query Match
 Best Local Similarity 26.0%; Score 13; DB 2; Length 21;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PN 2
 Db 10 PN 11

RESULT 16
 S05031
 cytochrome b559 component psbf - Synechococcus sp. (strain Copeland) (fragment)
 N:Alternate names: photosystem II 5.4K protein
 C:Species: Synechococcus sp.
 C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 16-Feb-1997
 C:Accession: S05031
 R:Ikemuhl, M.; Koike, H.; Inoue, Y.
 FEBS Lett. 251, 155-160, 1989
 A:Title: Identification of psbI and psbL gene products in cyanobacterial photosystem II
 A:Reference number: S05030
 A:Accession: S05031
 A:Molecule type: protein
 A:Residues: 1-21 <IRE>
 A:Note: the source is designated as Synechococcus vulcanus
 C:Genetics:
 A:Gene: psbP
 C:Keywords: transmembrane protein

Query Match
 Best Local Similarity 26.0%; Score 13; DB 2; Length 21;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PN 2
 Db 5 PN 6

RESULT 17
 E41316
 hypothetical protein (fla 3' region) - Methanococcus voltae (fragment)
 C:Species: Methanococcus voltae
 C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 18-Jun-1993
 C:Accession: E41316
 R:Kaimakoff, M.L.; Jarrell, K.F.
 J. Bacteriol. 173, 7113-7125, 1991
 A:Title: Cloning and sequencing of a multigene family encoding the flagellins of Methanococcus voltae
 A:Reference number: A41316; MUID:92041608; PMID:1718944
 A:Accession: E41316
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-21 <KAL>
 A:Cross-references: GB:M72148

Query Match
 Best Local Similarity 26.0%; Score 13; DB 2; Length 21;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PN 2

Db 2 PN 3
 RESULT 18
 S03986
 agglutinin beta-1 chain - Osage orange
 C:Species: Maclura pomifera (Osage orange)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 01-Aug-1997
 C:Accession: S03986; S03988
 R:Young, N.M.; Johnston, R.A.Z.; Szabo, A.G.; Watson, D.C.
 Arch. Biochem. Biophys. 270, 596-603, 1989
 A:Title: Homology of the D-galactose-specific lectins from Artocarpus integrifolia an
 A:Reference number: S03983; MUID:89206218; PMID:2705782
 A:Accession: S03986
 A:Molecule type: protein
 A:Residues: 1-21 <YOD>
 A:Note: beta-1 form
 A:Accession: S03988
 A:Molecule type: protein
 A:Residues: 2-21 <YOD>
 A:Note: beta-3 form

Query Match
 Best Local Similarity 26.0%; Score 13; DB 2; Length 21;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PN 2
 Db 3 PN 4

RESULT 19
 S03481
 T-cell receptor alpha chain J region (7a20) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Nov-1999
 C:Accession: S03481
 R:Arden, B.; Klotz, J.L.; Sin, G.; Hood, L.E.
 Nature 316, 783-787, 1985
 A:Title: Diversity and structure of genes of the alpha family of mouse T-cell antigen
 A:Reference number: S03467; MUID:85296324; PMID:3839904
 A:Accession: S03481
 A:Molecule type: mRNA
 A:Residues: 1-21 <AKD>
 A:Cross-references: EMBL:X02975; NID:954392; PIDN:CAA26717.1; PID:9773240
 A:Note: this sequence was determined from the differentiated gene
 C:Keywords: T-cell receptor
 F:1-17/Domain: T-cell receptor alpha chain J region #status predicted <JRE>

Query Match
 Best Local Similarity 26.0%; Score 13; DB 2; Length 21;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PN 2
 Db 16 PN 17

RESULT 20
 A37111
 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain - spinach (fragment)
 C:Species: Spinacia oleracea (spinach)
 C:Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 12-Apr-1995
 C:Accession: A37111
 R:Sato, M.H.; Hisabori, T.; Yoshida, M.
 J. Biol. Chem. 265, 13419-13422, 1990
 A:Title: The 55-kDa polypeptide released from spinach thylakoid membranes with 1 M Li
 A:Reference number: A37111; MUID:90337936; PMID:2143183
 A:Accession: A37111
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <SAT>

C:Superfamily: ribulose-bisphosphate carboxylase small chain
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 24.0%; Score 12; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 7.3e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 11 YXXXXY 16
DB 12 YETLSY 17

RESULT 21

S03335
Photosystem II phosphoprotein psbH - Synechococcus sp. (strain Copeland) (fragment)
N:Alternate names: photosystem II 6.5K protein
C:Species: Synechococcus sp.
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Dec-1993
C:Accession: S03335
R:Koike, H.; Mamada, K.; Ikeuchi, M.; Inoue, Y.
FEBS Lett. 244, 391-396, 1989
A:Title: Low-molecular-mass proteins in cyanobacterial photosystem II: identification of
A:Reference number: S03335; MWID:89153587; PMID:2493396
A:Accession: S03335
A:Molecule type: protein
A:Residues: 1-20 <KOI>
A:Note: the source is designated as Synechococcus vulcanus
C:Genetics:
A:Gene: psbH
C:Superfamily: photosystem II phosphoprotein psbH
C:Keywords: phosphoprotein; photosynthesis; photosystem II; thylakoid

Query Match 24.0%; Score 12; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 7.3e+03;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NXXY 5
DB 14 NSEY 17

RESULT 22

P00300
Large protein - bovine respiratory syncytial virus (strain A51908) (fragment)
C:Species: bovine respiratory syncytial virus
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 08-Oct-1999
C:Accession: P00300
R:Zamora, M.; Samal, S.K.
J. Gen. Virol. 73, 737-741, 1992
A:Title: Sequence analysis of M2 mRNA of bovine respiratory syncytial virus obtained from
A:Reference number: J01481; MWID:92185490; PMID:1312130
A:Accession: P00300
A:Molecule type: mRNA
A:Residues: 1-20 <ZAM>
A:Cross-references: GB:M82816; NID:9210823; PIDN:AAA42807.1; PID:9210827
C:Genetics:
A:Gene: L

Query Match 24.0%; Score 12; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 7.3e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 11 YXXXXY 16
DB 13 YLTDSY 18

RESULT 23

S53440
glutathione-binding protein GST1 - blue mussel
C:Species: Mytilus edulis (blue mussel)
C>Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
C:Accession: S53440

R: Fitzpatrick, P.J.; Krag, T.O.B.; Hojrup, P.; Sheehan, D.
Biochem. J. 305, 145-150, 1995
A:Title: Characterization of a glutathione S-transferase and a related glutathione-bl
A:Reference number: S53440; MWID:95126896; PMID:7826322
A:Accession: S53440
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <FIT>

Query Match 24.0%; Score 12; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 7.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 PNXXY 5
DB 1 PTLVY 5

RESULT 24

JC5589
ribonuclease RCL2 (EC 3.1.27.-) peptide 2 - bullfrog
N:Alternate names: ribonuclease RCL2 peptide 1
C:Species: Rana catesbeiana (bullfrog)
C>Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 07-May-1999
C:Accession: JC5589
R:Inokuchi, N.; Kobayashi, H.; Miyamoto, M.; Koyama, T.; Iwama, M.; Ohgi, K.; Irie, M
Biol. Pharm. Bull. 20, 471-478, 1997
A:Title: Primary structure of base non-specific and acid ribonuclease from bullfrog (
A:Reference number: JC5588; MWID:97322209; PMID:9178923
A:Accession: JC5589
A:Molecule type: protein
A:Residues: 1-20 <IN2>
A:Comment: This enzyme belongs to ribonuclease T2 family. This peptide 2 or peptide 1
C:Keywords: hydrolase
F:4-20/Product: peptide 1 #status experimental <PPI>

Query Match 24.0%; Score 12; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 7.3e+03;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NXXY 5
DB 12 NTVY 15

RESULT 25

A61276
Superoxide dismutase (EC 1.15.1.1) (Fe/Mn) homolog - chicken (fragment)
N:Alternate names: osteoclast membrane glycoprotein
C:Species: Gallus gallus (chicken)
C>Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 05-Mar-1999
C:Accession: A61276
R:Oursler, M.J.; Li, L.; Osodoby, P.
J. Cell. Biochem. 46, 219-233, 1991
A:Title: Purification and characterization of an osteoclast membrane glycoprotein wit
A:Reference number: A61276; MWID:92129474; PMID:1723067
A:Accession: A61276
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <OUR>
C:Function:
A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxyg
C:Keywords: metalloprotein; oxidoreductase

Query Match 24.0%; Score 12; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 7.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
DB 5 PDLRY 9

RESULT 26
S03954
acidic fibroblast growth factor - pig (fragment)
N:Alternate names: alpha-endothelial cell growth factor
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
C:Accession: S03954
R:Quinkler, W.; Maasberg, M.; Bernotat-Danielowski, S.; Luethe, N.; Sharma, H.S.; Schape
Eur. J. Biochem. 181, 67-73, 1989
A:Title: Isolation of heparin-binding growth factors from bovine, porcine and canine head
A:Reference number: S03953; MUID:89231704; PMID:2714282
A:Accession: S03954
A:Molecule type: protein
A:Residues: 1-20 <QNT>
C:Keywords: growth factor

Query Match 24.0%; Score 12; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 7.3e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 PNXXY 5
1 1 1
5 PKLXY 9

RESULT 27
I65270
collagen alpha 1(I) chain - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 13-Aug-1999
C:Accession: I65270
R:Genovese, C.; Rowe, D.; Kream, B.
Biochemistry 23, 6210-6216, 1984
A:Title: Construction of DNA sequences complementary to rat alpha-1 and alpha-2 collagen
A:Reference number: I52392; MUID:85122694; PMID:6395893
A:Accession: I65270
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-21 <RES>
A:Cross-references: GB:M12200; NID:9203191; PIDN:AAA40835.1; PID:9203195
C:Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology

Query Match 24.0%; Score 12; DB 2; Length 21;
Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 NXXY 5
1 1 1
4 NITY 7

RESULT 28
I58423
arylhydrocarbon receptor - mouse
C:Species: Mus sp. (mouse)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: I58423
R:Minura, J.; Ema, M.; Sogawa, K.; Ikawa, S.; Fujii-Kuriyama, Y.
Pharmacogenetics 4, 349-354, 1994
A:Title: A complete structure of the mouse Ah receptor gene.
A:Reference number: I58423; MUID:95218835; PMID:7704041
A:Accession: I58423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-21 <RES>
A:Cross-references: GB:S76844; NID:9913085; PIDN:AAB33978.1; PID:9913086
C:Genetics:
A:Gene: Ah

Query Match 24.0%; Score 12; DB 2; Length 21;
Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NXXY 5
1 1 1
6 NITY 9

RESULT 29
B53875
creatine kinase (EC 2.7.3.2) CK-I - coho salmon (fragment)
C:Species: Oncorhynchus kisutch (coho salmon)
C>Date: 26-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1997
C:Accession: B53875
R:White, K.C.; Babbitt, P.C.; Buechler, D.D.; Kenyon, G.L.
J. Protein Chem. 11, 489-494, 1992
A:Title: The principal islet of the Coho salmon (Oncorhynchus kisutch) contains the BB
A:Reference number: A53875; MUID:93080727; PMID:1449598
A:Accession: B53875
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-20 <WHI>
A:Experimental source: Brockmann body, principal islet
A>Note: sequence extracted from NCBI backbone (NCBIP:120600)
C:Superfamily: creatine kinase; creatine kinase repeat homology
C:Keywords: phosphotransferase

Query Match 22.0%; Score 11; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.3e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 YXXXXX 11
1 1 1 1 1
13 YSAEXXY 19

RESULT 30
G61491
seed protein ws-25 - winged bean (fragment)
C:Species: Psophocarpus tetragonolobus (winged bean)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-2000
C:Accession: G61491
R:Hirano, H.
J. Protein Chem. 8, 115-130, 1989
A:Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two
A:Reference number: A61491; MUID:89351606; PMID:2765119
A:Accession: G61491
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <HIR>
C:Superfamily: plant knutiz-type proteinase inhibitor
C:Keywords: glycoprotein; seed

Query Match 22.0%; Score 11; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NXXY 5
1 1 1
15 NRGY 18

RESULT 31
A49048
T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragmen
C:Species: Homo sapiens (man)
C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: A49048
R:Stoud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.
Eur. J. Immunol. 22, 2413-2418, 1992
A:Title: Limited heterogeneity of T cell receptor variable region gene usage in juven
A:Reference number: A49048; MUID:92387250; PMID:1387614
A:Accession: A49048
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-20 <SIO>

A:Experimental source: patient EV, IL-2R+ synovial T-cells
A:Note: sequence extracted from NCBI backbone (NCBI:P113263)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 22.0%; Score 11; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 NXXY 5
| |
Db 14 NXXY 17

RESULT 32
PS0087
Microbial serine proteinase (EC 3.4.21.-) TH - Bacillus thuringiensis subsp. kurstaki (H
C:Species: Bacillus thuringiensis subsp. kurstaki
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 31-Dec-1993
C:Accession: PS0087
R:Kunitzate, A.; Okamoto, M.; Ohmori, I.
Agric. Biol. Chem. 53, 3251-3256, 1989
A:Title: Purification and characterization of a thermostable serine protease from Bacill
A:Reference number: PS0087
A:Accession: PS0087
A:Molecule type: protein
A:Residues: 1-20 <KUN>
C:Comment: This protein is a thermostable proteinase.
C:Comment: The proteolytic activity is inhibited both by an active-site inhibitor of ser
C:Keywords: hydrolase; serine proteinase

Query Match 22.0%; Score 11; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 NXXY 5
| |
Db 9 NXXY 12

RESULT 33
S61281
Probable L-histidine aminotransferase, nikkomycin-synthesizing - Streptomyces tendae (fr
C:Species: Streptomyces tendae
C:Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 07-May-1999
C:Accession: S61281
R:Moehrle, V.; Roos, U.; Bormann, C.
Mol. Microbiol. 15, 561-571, 1995
A:Title: Identification of cellular proteins involved in nikkomycin production in Strept
A:Reference number: S61278; MUID:95302967; PMID:7783626
A:Accession: S61281
A:Molecule type: protein
A:Residues: 1-20 <MOE>

Query Match 22.0%; Score 11; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 NXXY 5
| | | |
Db 7 NXXY 10

RESULT 34
A57106
hull allergen Gly m 2 - soybean (fragment)
C:Species: Glycine max (soybean)
C:Date: 27-Oct-1995 #sequence_revision 27-Oct-1995 #text_change 25-Oct-1996
C:Accession: A57106
R:Codina, R.; Swanson, M.C.; Fernandez-Caldas, E.; Lockey, R.F.; Trudeau, W.L.; Rama, R.
submitted to the Protein Sequence Database, October 1995
A:Description: Partial sequence of the Gly m 2 allergen from soybean hull.
A:Reference number: A57106

A:Accession: A57106
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <COD>
A:Experimental source: seed episperm
C:Keywords: seed

Query Match 22.0%; Score 11; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 PNXXY 5
| |
Db 8 PADTY 12

RESULT 35
D49255
T-cell receptor beta chain V-D-J-C region (V beta 12, J beta 2.4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: D49255
R:Rosenberg, W.M.; Moss, P.A.; Bell, J.I.
Eur. J. Immunol. 22, 541-549, 1992
A:Title: Variation in human T cell receptor V beta and J beta repertoire: analysis us
A:Reference number: A49039; MUID:92104737; PMID:1311263
A:Accession: D49255
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-20 <ROS>
A:Note: sequence extracted from NCBI backbone (NCBI:P:90725)
C:Keywords: T-cell receptor

Query Match 22.0%; Score 11; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 NXXY 5
| |
Db 15 NIOY 18

RESULT 36
S03508
T-cell receptor alpha chain J region (19) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 05-Nov-1999
C:Accession: S03508
R:Winkler, A.; Molanese, S.; Hood, L.
Nature 316, 832-836, 1985
A:Title: Genomic organization of the genes encoding mouse T-cell receptor alpha-chain
A:Reference number: S03503; MUID:85296332; PMID:2993908
A:Accession: S03508
A:Molecule type: DNA
A:Residues: 1-20 <WIN>
A:Cross-references: EMBL:X03058; NID:954521; PIDN:CAA26865.1; PID:e7559; PID:g1334132
A:Note: this sequence was determined from the germline gene
C:Keywords: T-cell receptor

Query Match 22.0%; Score 11; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 NXXY 5
| |
Db 5 NYXY 8

RESULT 37
S44465
pyrrocoricin - Pyrrocoris apterus
C:Species: Pyrrocoris apterus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999

C:Accession: S44465
 R:Coccianich, S.; Dupont, A.; Hegy, G.; Lanot, R.; Holder, F.; Hetru, C.; Hoffmann, J.A.
 Biochem. J. 300, 567-575, 1994
 A:Title: Novel inducible antibacterial peptides from a hemipteran insect, the sap-sucking
 A:Reference number: S44463; MUID:94271176; PMID:8002963
 A:Accession: S44465
 A:Molecule type: protein
 A:Residues: 1-20 <COC>
 C:Function:
 A:Description: antibacterial protein
 A:Note: active against Gram-negative bacteria
 C:Keywords: antibacterial; hemolymph; immune response

Query Match 22.0%; Score 11; DB 2; Length 20;
 Best Local Similarity 40.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 NXXY 5
 DB 13 PPRY 17

RESULT 38
 A61487
 110K ATPase, intestinal - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
 C:Accession: A61487
 R:Atkinson, M.A.L.; Collins, J.H.
 J. Protein Chem. 8, 495-498, 1989
 A:Title: Sequence similarities between chicken intestinal 110-kDa ATPase and myosin I-11
 A:Reference number: A61487; MUID:90026831; PMID:2529866
 A:Accession: A61487
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-21 <ATK>
 C:Superfamily: brush border myosin heavy chain I; myosin motor domain homology
 C:Keywords: intestine

Query Match 22.0%; Score 11; DB 2; Length 21;
 Best Local Similarity 50.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NXXY 5
 DB 12 NRY 15

RESULT 39
 S02643
 RNA-directed RNA polymerase (EC 2.7.7.48) - tobacco mosaic virus (fragment)
 N:Alternate names: RNA replicase
 C:Species: tobacco mosaic virus, TMV
 C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 30-Sep-1993
 C:Accession: S02643
 R:Mesli, T.; Motoyoshi, F.; Adachi, A.; Watanabe, Y.; Takamatsu, N.; Okada, Y.
 EMBO J. 7, 1575-1581, 1988
 A:Title: Two concomitant base substitutions in the putative replicase genes of tobacco m
 A:Reference number: S02643
 A:Accession: S02643
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-21 <MES>
 C:Genetics:
 A:Gene: Tm-1
 C:Superfamily: cucumber mosaic virus RNA 1 protein
 C:Keywords: nucleotidyltransferase

Query Match 22.0%; Score 11; DB 2; Length 21;
 Best Local Similarity 50.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NXXY 5

DB 5 NORX 8

RESULT 40
 S49040
 dps-protein 19K - Escherichia coli (fragment)
 C:Species: Escherichia coli
 C>Date: 27-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
 C:Accession: S49040
 R:Altuvia, S.; Almitron, M.; Hulsman, G.; Kolter, R.; Storz, G.
 Mol. Microbiol. 13, 265-272, 1994
 A:Title: The dps promoter is activated by OxyR during growth and by IHF and sigma(s)
 A:Reference number: S49040; MUID:95075312; PMID:7984106
 A:Accession: S49040
 A:Molecule type: protein
 A:Residues: 1-21 <ALT>
 C:Genetics:
 A:Gene: dps

Query Match 22.0%; Score 11; DB 2; Length 21;
 Best Local Similarity 50.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NXXY 5
 DB 14 NLXY 17

RESULT 41
 S01816
 hemoglobin BIV - tube worm (Lamellibrachia sp.) (fragment)
 C:Species: Lamellibrachia sp.
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Jun-1993
 C:Accession: S01816
 R:Suzuki, T.; Takagi, T.; Ohta, S.
 Biochem. J. 255, 541-545, 1988
 A:Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarka
 A:Reference number: S01807; MUID:89076216; PMID:3302832
 A:Accession: S01816
 A:Molecule type: protein
 A:Residues: 1-21 <S02>

Query Match 22.0%; Score 11; DB 2; Length 21;
 Best Local Similarity 50.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NXXY 5
 DB 17 NQRY 20

RESULT 42
 PNO133
 pepsin (EC 3.4.23.-) 1 - horse (fragment)
 N:Alternate names: Pepsin (pI 1.8)
 C:Species: Equus caballus (domestic horse)
 C>Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 07-May-1999
 C:Accession: PNO133
 R:Gonchar, M.V.; Lavrenova, G.I.; Rudenskaya, G.N.; Galda, A.V.; Stepanov, V.M.
 Biochimica 49, 1026-1037, 1984
 A:Title: Multiple forms of horse pepsin.
 A:Reference number: PNO133; MUID:84281135; PMID:6432065
 A:Accession: PNO133
 A:Molecule type: protein
 A:Residues: 1-20 <GON>
 A:Note: article in Russian with English abstract
 C:Superfamily: pepsin
 C:Keywords: aspartic proteinase; hydrolase; protein digestion

Query Match 20.0%; Score 10; DB 2; Length 20;
 Best Local Similarity 33.3%; Pred. No. 2.3e+04;
 Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 11 YXXXXX 16
|
|
DB 9 YMDSEY 14

RESULT 43

A05332
serum amyloid P-component - plaiice (fragment)
N:Alternate names: SAP
C:Species: Pleurocetes plateasa (plaiice)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 22-Apr-1995
C:Accession: A05332
R:Peys, M.B.; de Beer, F.C.; Milstein, C.P.; March, J.F.; Feinstein, A.; Butress, N.; C
Biochim. Biophys. Acta 704, 123-133, 1982
A:Reference number: A90642; MUID:82232106; PMID:7093286
A:Contents: tentative sequence
A:Accession: A05332
A:Molecule type: protein
A:Residues: 1-20 <PEP>
C:Superfamily: C-reactive protein
C:Keywords: amyloid; glycoprotein; pentraxin; plasma

Query Match 20.0%; Score 10; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.3e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
|
|
DB 18 PB.19

RESULT 44

PL0161
hemagglutinin - Influenza H2N2 (fragment)
C:Species: influenza H2N2
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-May-1997
C:Accession: PL0161
R:Sweeter, M.T.; Braciale, V.L.; Braciale, T.J.
J. Exp. Med. 170, 1357-1368, 1989
A:Title: Class I major histocompatibility complex-restricted T lymphocyte recognition of
A:Reference number: PL0161; MUID:90010790; PMID:2477491
A:Accession: PL0161
A:Molecule type: mRNA
A:Residues: 1-20 <SWE>
A:Experimental source: strain A/JAP/305/57
C:Comment: This protein plays a major role in initiation of infection and in the pathoge
C:Superfamily: influenza virus hemagglutinin
C:Keywords: hemagglutinin
F:1-20/Region: immunodominant site recognized by T-lymphocytes

Query Match 20.0%; Score 10; DB 2; Length 20;
Best Local Similarity 28.6%; Pred. No. 2.3e+04;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 YXXXXX 11
|
|
DB 4 YONVGT 10

RESULT 45

P00046
citrate (sl)-synthase (EC 4.1.3.7) - Streptomyces hygroscopicus (fragment)
N:Alternate names: citrate condensing enzyme; citrogenase; condensing enzyme; oxaloaceta
C:Species: Streptomyces hygroscopicus
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 05-May-2000
C:Accession: P00046
R:Shimochino, K.W.; Imai, S.; Murakami, T.; Seto, H.
Agric. Biol. Chem. 54, 463-470, 1990
A:Title: Purification and characterization of citrate synthase from Streptomyces hygrosc
A:Reference number: P00106; MUID:90334852; PMID:1368511
A:Accession: P00046
A:Molecule type: protein

A:Residues: 1-20 <SHI>
A:Experimental source: strain SF-1293
C:Comment: This enzyme catalyzes the synthesis of citric acid.
C:Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase; tricarboxylic acid cycle

Query Match 20.0%; Score 10; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.3e+04;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 11 YXXXXX 16
|
|
DB 9 YGDSEY 14

RESULT 46

A47105
dystroglycan - chicken (fragment)
N:Alternate names: laminin-binding protein 120
C:Species: Gallus gallus (chicken)
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C:Accession: A47105
R:Gee, S.H.; Blacher, R.W.; Douville, P.J.; Provost, P.R.; Yurchenco, P.D.; Carbonett
J. Biol. Chem. 268, 14972-14980, 1993
A:Title: Laminin-binding protein 120 from brain is closely related to the dystrophin-
A:Reference number: A47105; MUID:93315474; PMID:8325873
A:Accession: A47105
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <GEE>
A:Experimental source: embryonic brain
A:Note: sequence extracted from NCBI backbone (NCBIP:134982)
C:Keywords: heparin binding

Query Match 20.0%; Score 10; DB 2; Length 20;
Best Local Similarity 20.0%; Pred. No. 2.3e+04;
Matches 1; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
|
|
DB 15 PDSSH 19

RESULT 47

S37684
protein IEF SSP 9125 - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 09-Dec-1993 #sequence_revision 17-Nov-1995 #text_change 17-Nov-1995
C:Accession: S37684
R:Jeffers, H.; Madsen, P.; Rasmussen, H.H.; Honore, B.; Andersen, A.H.; Walbum, E.; V
J. Mol. Biol. 231, 982-998, 1993
A:Title: Molecular cloning and expression of the transformation sensitive epithelial
A:Reference number: S34753; MUID:93294871; PMID:8515476
A:Accession: S37684
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <LEF>

Query Match 20.0%; Score 10; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.3e+04;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 11 YXXXXX 16
|
|
DB 14 YKVFY 19

RESULT 48

A85659
hypothetical protein Z1618 [imported] - Escherichia coli (strain O157:H7, substrain E
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: A85659; H85607

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grobecek, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: AB5659
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-20 <STO>
 A:Cross-references: GB:AE005174; NID:q12514504; PIDN:AGS55733.1; GSPDB:GN00145; UWGP:Z16
 A:Experimental source: strain O157:H7, substrain EDL933
 A:Accession: H85607
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-20 <ST2>
 A:Cross-references: GB:AE005174; NID:q12514504; PIDN:AGS55324.1; GSPDB:GN00145; UWGP:Z11
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: Z1618; Z1179

Query Match 20.0%; Score 10; DB 2; Length 20;
 Best Local Similarity 40.0%; Pred. No. 2.3e+04;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 PNXXY 5
 DB 2 PVNSY 6

RESULT 49

PH1688
 Ig heavy chain V region (clone NP-7-1) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
 C:Accession: PH1688
 R:McHeyzer-Williams, M.G.; Mclean, M.J.; Lalor, P.A.; Nossal, G.J.V.
 J. Exp. Med. 178, 295-307, 1993
 A>Title: Antigen-driven B cell differentiation in vivo.
 A:Reference number: PH1675; MUID:93301607; PMID:8315385
 A:Accession: PH1688
 A:Molecule type: mRNA
 A:Residues: 1-21 <MCH>
 A:Experimental source: B cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin

Query Match 20.0%; Score 10; DB 2; Length 21;
 Best Local Similarity 33.3%; Pred. No. 2.4e+04;
 Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 11 YXXXXY 16
 DB 16 YYPYRY 21

RESULT 50

PD0015
 actin-binding protein - Tetrahymena pyriformis (fragment)
 C:Species: Tetrahymena pyriformis
 C:Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jun-2000
 C:Accession: PD0015
 R:Watanabe, A.; Kurasawa, Y.; Watanabe, Y.; Numata, O.
 J. Biochem. 123, 607-613, 1998
 A>Title: A new Tetrahymena actin-binding protein is localized in the division furrow.
 A:Reference number: PD0015; MUID:98207047; PMID:9538250
 A:Accession: PD0015
 A:Molecule type: protein
 A:Residues: 1-21 <MAT>
 C:Genetics:
 A:Genetic code: SGC5
 C:Superfamily: plastin; alpha-actinin actin-binding domain homology; calmodulin repeat
 C:Keywords: EF hand

Query Match 20.0%; Score 10; DB 2; Length 21;
 Best Local Similarity 50.0%; Pred. No. 2.4e+04;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NXXY 5
 DB 9 NHPY 12

Search completed: June 11, 2003, 07:44:21
 Job time : 21 secs

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OM protein - protein search, using sw model

Run on: June 11, 2003, 07:42:19 ; Search time 11 Seconds
(without alignments)
79.182 Million cell updates/sec

Title: US-09-883-727A-127

Perfect score: 50
Sequence: 1 PNXXXXXXXYYYYYYYYX 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 202

Minimum DB seq length: 20
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	13	26.0	20	1	AROO_AMYME
2	13	26.0	20	1	HGLI_FASHE
3	13	26.0	20	1	LECI3_MACPO
4	13	26.0	20	1	RT16_BOVIN
5	13	26.0	20	1	TL19_SPIOL
6	13	26.0	21	1	CPFA_TREPH
7	13	26.0	21	1	FIBB_ANTAM
8	13	26.0	21	1	LECI1_MACPO
9	13	26.0	21	1	PSBF_SYNVU
10	13	26.0	21	1	RL21_HALCU
11	13	26.0	21	1	YFLA_METVO
12	12	24.0	20	1	PSBH_SYNVU
13	12	24.0	20	1	SODM_HORVU
14	12	24.0	21	1	HPAA_STRGD
15	12	24.0	21	1	TL19_ARATH
16	11	22.0	20	1	CAT4_FASHE
17	11	22.0	20	1	FIBR_PACLE
18	11	22.0	20	1	PYRR_PYRAP
19	11	22.0	20	1	SCI8_MESMA
20	10	20.0	20	1	CISY_STRHY
21	10	20.0	20	1	MCRG_METTE
22	10	20.0	20	1	SAMP_PLEBL
23	10	20.0	21	1	PAW1_TETPY
24	10	20.0	21	1	LE04_BIOGL
25	9	18.0	20	1	SODF_PASPI
26	9	18.0	20	1	YOH4_KLEAE
27	8	16.0	20	1	ACPH_BOVIN
28	8	16.0	20	1	BULB_NARPS
29	8	16.0	20	1	CAT1_FASHE
30	8	16.0	20	1	CHP_THICU
31	8	16.0	20	1	COGI_CHIOP
32	8	16.0	20	1	COXM_THUOB
33	8	16.0	20	1	COXN_THUOB

34	8	16.0	20	1	CP35_PAPSP	P80056 papio sp. (
35	8	16.0	20	1	F1BB_ELEMA	P14538 elephas max
36	8	16.0	20	1	HELT_HELLO	P46693 heloderma h
37	8	16.0	20	1	LEP2_HUMAN	P56642 homo sapien
38	8	16.0	20	1	MTF_PIG	P80928 sus scrofa
39	8	16.0	20	1	NITI1_HELAN	P82007 helianthus
40	8	16.0	20	1	R1PX_CUCPE	P80750 cucurbita p
41	8	16.0	20	1	UCRQ_EQUAR	P81247 equisetum a
42	8	16.0	20	1	VR90_BORPE	P81549 bordelella
43	8	16.0	20	1	VSP1_TRIOK	P20005 trimeresuru
44	8	16.0	21	1	ALL7_OLEEU	P81430 olea europa
45	8	16.0	21	1	FEDB_AMEYE	P80706 amycolatops
46	8	16.0	21	1	GERP_WHEAT	P29532 triticum ae
47	8	16.0	21	1	MCT3_MOUSE	P21843 mus musculu
48	8	16.0	21	1	NEPH_RAT	P58522 rattus norv
49	8	16.0	21	1	NRLA_ACISP	P33036 actinobact
50	8	16.0	21	1	SCIB_BPTS	P22208 bacterioph
51	8	16.0	21	1	TERI_APTME	P36587 apis mellif
52	7	14.0	20	1	ALBG_EQUAS	P33090 equus asinu
53	7	14.0	20	1	ABP_PIG	O91rc7 sus scrofa
54	7	14.0	20	1	APAI_ERYPA	P18647 erythrocyb
55	7	14.0	20	1	ATP4_SPIOL	P80085 spinacia ol
56	7	14.0	20	1	B1P_BHAVU	P80089 phaseolus v
57	7	14.0	20	1	CAQS_RAT	P19633 rattus norv
58	7	14.0	20	1	CD4_SHEEP	P05542 ovis aries
59	7	14.0	20	1	COG1_PARC	P20731 parallithode
60	7	14.0	20	1	COG2_CHIOP	P34154 chionocete
61	7	14.0	20	1	COG3_CHIOP	P34155 chionocete
62	7	14.0	20	1	COG4_CHIOP	P34156 chionocete
63	7	14.0	20	1	COGA_PARC	P20732 parallithode
64	7	14.0	20	1	COGB_PARC	P20733 parallithode
65	7	14.0	20	1	COGC_PARC	P20734 parallithode
66	7	14.0	20	1	COXA_THUOB	P80972 thunnus obe
67	7	14.0	20	1	COXB_THUOB	P80974 thunnus obe
68	7	14.0	20	1	COXF_ONCMY	P80329 oncorhynch
69	7	14.0	20	1	COXQ_ONCMY	P80330 oncorhynch
70	7	14.0	20	1	COXQ_THUOB	P80983 thunnus obe
71	7	14.0	20	1	CPXX_RHORH	P31718 rhodococcus
72	7	14.0	20	1	CRP_MUSCA	P19094 musculus ca
73	7	14.0	20	1	CS2I_STRTR	P81621 streptococc
74	7	14.0	20	1	CUDP_VERTH	P80406 verticilliu
75	7	14.0	20	1	DER6_DERPT	P49277 dermatophag
76	7	14.0	20	1	DFTS_RAT	P07148 rattus norv
77	7	14.0	20	1	ELAS_GADMO	P31947 gadus morhu
78	7	14.0	20	1	F1BB_FELCA	P14469 felis silve
79	7	14.0	20	1	F1BB_SHEEP	P14470 ovis aries
80	7	14.0	20	1	FLAW_AZOVI	P52964 azotobacter
81	7	14.0	20	1	FRHA_METBA	P80489 methanosarc
82	7	14.0	20	1	GTS2_ASCSU	P84829 aecaris suu
83	7	14.0	20	1	ITRA_ALBUU	P24925 albizia ju
84	7	14.0	20	1	JHBP_BOMMO	P16127 bombyx mori
85	7	14.0	20	1	KORA_MERTM	P80904 methanobact
86	7	14.0	20	1	LEC2_MACPO	P18676 meclura pom
87	7	14.0	20	1	LEC3_ARTIN	P18677 artocarpus
88	7	14.0	20	1	LECB_IRIHO	P56643 iris hollan
89	7	14.0	20	1	LPP3_HUMAN	P56644 homo sapien
90	7	14.0	20	1	MDH_KIBAR	P19978 kibdelospor
91	7	14.0	20	1	MDH_MICGL	P19979 kibdelospor
92	7	14.0	20	1	M117_BOVIN	P35451 bos taurus
93	7	14.0	20	1	NEUA_RAT	P29188 rattus norv
94	7	14.0	20	1	OAR_PHOPE	P14803 photinus py
95	7	14.0	20	1	OMPI_ACTAC	P20242 actinobacil
96	7	14.0	20	1	OXLA_CROAT	P56742 crocatalus at
97	7	14.0	20	1	PCWG_PACGO	P82428 pachycondyl
98	7	14.0	20	1	PEPT_FUSNP	P81207 fusobacteri
99	7	14.0	20	1	PEK_CLOPA	P81346 clostridium
100	7	14.0	20	1	PNV2_PHONI	P81346 clostridium
101	7	14.0	20	1	PSAF_MAIZE	P31393 zea mays (m
102	7	14.0	20	1	PSAF_PEA	P20119 pisum sativ
103	7	14.0	20	1	PSAL_SYNVU	P25937 synechococc
104	7	14.0	20	1	PURK_RHOSH	O33121 rhodobacter
105	7	14.0	20	1	PYRX_PSEFI	P56586 pseudomonas
106	7	14.0	20	1	RECX_AZOVI	P37863 azotobacter

107	7	14.0	20	1	RLCI_HALMA	P12740	halarcuola
108	7	14.0	20	1	RNMD_PIG	P80551	zea scrofa
109	7	14.0	20	1	SB60_MAZE	P82688	zea mays (m
110	7	14.0	20	1	SCBI_CANPA	P99507	scabi fami1
111	7	14.0	20	1	STRV_SYCL	P81470	steyla clav
112	7	14.0	20	1	SYR_RAT	P40329	rattus norv
113	7	14.0	20	1	THIO_CANPA	P99505	canis fami1
114	7	14.0	20	1	TL14_SPIOL	P82682	spiniacia o1
115	7	14.0	20	1	TL18_SPIOL	P82536	spiniacia o1
116	7	14.0	20	1	TL22_SPIOL	P82596	spiniacia o1
117	7	14.0	20	1	TRV6_ECOLI	P33389	escherichia
118	7	14.0	20	1	TRV6_ECOLI	P80420	strepptomyc
119	7	14.0	20	1	UN05_PINPS	P81674	pinus pinas
120	7	14.0	20	1	VMO2_CHICK	Q93849	gallus gall
121	7	14.0	20	1	VSP1_AGBEI	P33588	agkistrodon
122	7	14.0	20	1	YPER_SERMA	P22581	serratia ma
123	7	14.0	21	1	ATPB_PHYPA	P80658	physcomit
124	7	14.0	21	1	BOH1_BOMVA	P82282	domina var
125	7	14.0	21	1	BOH4_BOMVA	P82284	bomina var
126	7	14.0	21	1	BOH5_BOMVA	P82285	bomina var
127	7	14.0	21	1	BTX_ATRBI	P80163	atractaspis
128	7	14.0	21	1	CHIC_PEA	P31233	pisum sativ
129	7	14.0	21	1	CKXT_CONTU	P17684	conus tulip
130	7	14.0	21	1	ECDI_LYMDI	P80936	lymantria d
131	7	14.0	21	1	FER_PYRMO	P81638	pyrococcus
132	7	14.0	21	1	FIBB_BISBO	P14466	bison bonas
133	7	14.0	21	1	FIBB_BUBBU	P14467	bulbus bub
134	7	14.0	21	1	FIBB_CEREL	P14468	cervus elap
135	7	14.0	21	1	FIBB_MUNMU	P14475	munia m
136	7	14.0	21	1	FIBB_ODOHE	P1476	odocoleus
137	7	14.0	21	1	FIBB_RANTA	P14479	rangifer ta
138	7	14.0	21	1	FIBB_SYNCA	P14481	syncerus ca
139	7	14.0	21	1	GRX_BUNCN	P58305	bundosa
140	7	14.0	21	1	GYRA_STRSH	P50071	strepdomyc
141	7	14.0	21	1	LEC2_ARTIN	P18672	artocarpus
142	7	14.0	21	1	LPRM_CORDI	P21332	corneabacte
143	7	14.0	21	1	MDH_BURCE	P80537	burholderi
144	7	14.0	21	1	MDH_PSEIN	P80538	pseudomonas
145	7	14.0	21	1	MUL1_LITGE	P82066	litoria gen
146	7	14.0	21	1	ODP2_SOLTL	P81421	solanum tub
147	7	14.0	21	1	OMP1_ACTPL	P80368	actinobacil
148	7	14.0	21	1	OMP1_HAEPR	P80369	haemophilus
149	7	14.0	21	1	OMP4_PASHA	P80328	pasteurella
150	7	14.0	21	1	PII3_ECOLI	P13948	escherichia

ALIGNMENTS

RESULT 1
AROC_AMEYE STANDARD; PRT; 20 AA.
ID AROC_AMEYE
AC P46380;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-dehydroquininate dehydratase (EC 4.2.1.10) (3-dehydroquinase)
DE (Type II DHQase) (Fragment).
CN AROC
OS Amycolatopsis methanolica.
OC Bacteria; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Pseudonocardiales; Pseudonocardaceae;
OC Amycolatopsis.
OX NCBI_TaxID=1814;
RN (1)
RP SEQUENCE.
RC STRAIN=NCIB 11946;
RX MEDLINE=93123995; PubMed=1479361;
RA Euvierink G.J.W., Hessel G.I., Vrijbloed J.W., Coggins J.R.,
RA Dijkhuizen L.;
RT "Purification and characterization of a dual function
3-dehydroquininate dehydratase from Amycolatopsis methanolica.";
RL J. Gen. Microbiol. 138:2449-2457 (1992).

CC -1- FUNCTION: CATALYZE A TRANS-DEHYDRATION VIA AN ENOLATE
CC INTERMEDIATE. IS INVOLVED IN BOTH THE CATABOLISM OF QUINATE AND
CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS. HAS A TEMPERATURE
CC OPTIMAL OF 76 DEGREES CELSIUS AND PH OPTIMAL OF 9.0. TYPE II
CC ENZYMES ARE THERMOSTABLE.
CC -1- CATALYTIC ACTIVITY: 3-dehydroquininate = 3-dehydroshikimate + H(2)O.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC third step.
CC -1- SIMILARITY: BELONGS TO THE TYPE-II 3-DEHYDROQUININASE FAMILY.
CC -1- SIMILARITY: BELONGS TO THE TYPE-II 3-DEHYDROQUININASE FAMILY.
DR InterPro: IPR001874; DHQinase-II.
DR Pfam: PF01220; DHQinase-II; 1.
DR PROSITE: PS01029; DEHYDROQUININASE-II; PARTIAL.
KW Quinate metabolism; Aromatic amino acid biosynthesis; Lyase.
FT NON TER
SQ SEQUENCE 20 AA; 2197 MW; C24AA183E5CFDFOA CRC64;

Query Match Score 13; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
DB 9 PN 10

RESULT 2
HGL1_FASHE STANDARD; PRT; 20 AA.
ID HGL1_FASHE
AC P80527;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hemoglobins-like protein 1 (EC 3.4.22.34) (Newly excysted juvenile
DE protein 3) (Fragment).
OS Fasciola hepatica (liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomata; Fasciolidae; Fasciolidae;
OX NCBI_TaxID=6192;
RN (1)
RP SEQUENCE.
RX MEDLINE=95366993; PubMed=7639732;
RA Tkalcic J., Aszman K., Meusen E.;
RT "Fasciola hepatica: rapid identification of newly excysted juvenile
RT proteins.";
RL Biochem. Biophys. Res. Commun. 213:169-174 (1995).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of proteins and small-molecule
CC substrates at -Asn-|-Xaa-bonds.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT THE NEWLY EXCYSTED JUVENILE
CC STAGE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C13.
DR MEROPS: C13.003; -.
DR InterPro: IPR001096; Legumain.
DR Pfam: PF01650; Peptidase_C13; 1.
KW Hydrolyase; Thiol protease.
FT NON TER
SQ SEQUENCE 20 AA; 2278 MW; 865F368A1A03874D CRC64;

Query Match Score 13; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
DB 14 PN 15

RESULT 3
LEC3_MACPO STANDARD; PRT; 20 AA.
ID LEC3_MACPO
AC P18677;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-AUG-1991 (Rel. 19, Last annotation update)
 DE Agglutinin beta-3 chain (MPA).
 OS Maculura pomifera (Osage orange).
 CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eustosids I; Rosales; Moraceae; MacIura.
 NCBI_TaxID=3496;
 OK NCB1
 RN SEQUENCE.
 RP TISSUE=Seed;
 RC MEDLINE=89206218; PubMed=2705782;
 RA Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;
 RT "Homology of the D-galactose-specific lectins from Artocarpus
 integrifolia and MacIura pomifera and the role of an unusual small
 RT polypeptide subunit."
 RL Arch. Biochem. Biophys. 270:596-603 (1989).
 CC -1- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN
 CC STRUCTURE GAL-BETA1-3-GALNAC.
 CC -1- SUBUNIT: FORMED OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.
 CC -1- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.
 DR PIR: S03988; S03988.
 DR HSSP: P18676; 1JOT.
 KW Lectin.
 SQ SEQUENCE 20 AA; 2082 MW; AA38611BBD6370E0 CRC64;

Query Match 26.0%; Score 13; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 DB 2 PN 3

RESULT 4
 ID RT16_BOVIN STANDARD; PRT; 20 AA.
 AC P82915;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mitochondrial 28S ribosomal protein S16 (MRP-S16) (Fragments).
 GN RPS16.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 OK NCB1
 RN SEQUENCE.
 RP TISSUE=Liver;
 RC MEDLINE=21276436; PubMed=11279123;
 RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
 RT "The small subunit of the mammalian mitochondrial ribosome:
 RT Identification of the full complement of ribosomal proteins present."
 RL J. Biol. Chem. 276:19363-19374 (2001).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR000307; Ribosomal_S16.
 DR Pfam: PF00886; Ribosomal_S16; PARTIAL.
 DR PROSITE: PS00732; RIBOSOMAL_S16; PARTIAL.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 1
 FT NON_TER 10
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2205 MW; BC042AC57F236CES CRC64;

Query Match 26.0%; Score 13; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 3 PN 4

RESULT 5
 ID TL19_SPIOL STANDARD; PRT; 20 AA.
 AC P82799;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thylakoid lumenal 18.4 kDa protein (P18.4) (Fragment).
 OS Spinacia oleracea (Spinach).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 NCBI_TaxID=33562;
 OK NCB1
 RN SEQUENCE.
 RP Kieselbach T., Pettersson U., Bystedt M., Schroeder W.P.;
 RA Submitted (JUL-2000) to the SWISS-PROT data bank.
 RL -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
 KW Chloroplast; Thylakoid.
 FT NON_TER 20
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2130 MW; 460408C32420991B CRC64;

Query Match 26.0%; Score 13; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 DB 5 PN 6

RESULT 6
 ID CFPA_TREPH STANDARD; PRT; 21 AA.
 AC P56738;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cytoplasmic filament protein A (Fragment).
 GN CFPA.
 OS Treponema phagedenis.
 CC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 NCBI_TaxID=162;
 OK NCB1
 RN SEQUENCE.
 RP STRAIN=Kazan 5;
 RC MEDLINE=96236033; PubMed=8655496;
 RA You Y., Elmore S., Colton L.L., Mackenzie C., Stoops J.K.,
 RA Weinstock G.M., Norris S.J.;
 RT "Characterization of the cytoplasmic filament protein gene (cfpa) of
 RT Treponema pallidum subsp. pallidum."
 RL J. Bacteriol. 178:3177-3187 (1996).
 CC -1- FUNCTION: COMPONENT OF THE CYTOPLASMIC FILAMENTS THAT RUN THE
 CC LENGTH OF THE ORGANISM JUST UNDERNEATH THE CYTOPLASMIC MEMBRANE.
 CC -1- SUBCELLULAR LOCATION: AN ARRAY OF 4 TO 6 FILAMENTS LIE IN CLOSE
 CC APPosition TO THE INNER MEMBRANE AND ARE ALWAYS LOCALIZED DIRECTLY
 CC UNDERNEATH THE CORRESPONDING GROUP OF PERIPLASMIC FLAGELLA.
 KW Structural protein; Antigen.
 FT NON_TER 21
 FT NON_TER 21
 SQ SEQUENCE 21 AA; 2231 MW; 574604B4FPC2D017 CRC64;

Query Match 26.0%; Score 13; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 DB 9 PN 10

RESULT 7
FIBB_ANTAM STANDARD; PRT; 21 AA.
AC P14465;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Antilocapra americana (Pronhorn).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Antilocapridae; Antilocapra.
OX NCBI_TaxID=9891;
RN [1]
RP SEQUENCE.
RA "Moses G.A., Doolittle R.F.;
RT "Amino acid sequence studies on aridodactyl fibrinopeptides.";
RL Arch. Biochem. Biophys. 122:674-684(1967).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR InterPro: IPR002181; Fibrinogen C.
DR PROSITE: PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KM Blood coagulation; Plasma; Sulfation.
FT PEPTIDE 1 21 FIBRINOPEPTIDE B.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 21 21 SULFATION.
SQ SEQUENCE 21 AA; 2585 MW; FCE6183BE1F31627 CRC64;

Query Match 26.0%; Score 13; DB 1; Length 21;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
DB 2 PSYDY 6

RESULT 8
LECT1_MACPO STANDARD; PRT; 21 AA.
ID LECT1_MACPO
AC P18675;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Agglutinin beta-1 chain (MPA).
OS Maciura pomifera (Osage orange).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Rosales; Moraceae; Maciura.
OX NCBI_TaxID=3496;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed; PubMed=2705782;
RX Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;
RA "Homology of the D-galactose-specific lectins from Artocarpus
RT integrifolia and Maciura pomifera and the role of an unusual small
RT polypeptide subunit";
RL Arch. Biochem. Biophys. 270:596-603(1989).
CC -1- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN
CC STRUCTURE GAL-BETA1-3-GALNAc.
CC -1- SUBUNIT: FORMED OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.
CC -1- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.
DR PIR; S03986; S03986.

DR HSSP; P18676; 1JOT.
KM Lectin.
SQ SEQUENCE 21 AA; 2196 MW; AA38811BC1BFD0E0 CRC64;

Query Match 26.0%; Score 13; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
DB 3 PN 4

RESULT 9
PSBF_SYNVU STANDARD; PRT; 21 AA.
ID PSBF_SYNVU
AC P12239;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome B559 beta chain (Fragment).
GN PSBF.
OS Synecococcus vulcanus (Thermosynechococcus vulcanus).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=32053;
RN [1]
RP SEQUENCE.
RA Ikeuchi M., Koike H., Inoue Y.;
RT "Identification of pbsi and pbsl gene products in cyanobacterial
RT photosystem II reaction center preparation";
RL FEBS Lett. 251:155-160(1989).
CC -1- FUNCTION: THIS B-TYPE CYTOCHROME IS TIGHTLY ASSOCIATED WITH THE
CC REACTION CENTER OF PHOTOSYSTEM II AND POSSIBLY IS PART OF THE
CC WATER-OXIDATION COMPLEX.
CC -1- SUBUNIT: DIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE PSBE / PSBF FAMILY.
DR PIR; S05031; S05031.
DR InterPro: IPR001417; Cyt b559.
DR PROSITE: PS00537; CYTOCHROME B559; PARTIAL.
KM Photosystem II; Heme; Electron transport; Transmembrane.
FT DOMAIN 1 18 STROMAL (POTENTIAL).
FT TRANSMEM 19 >21 POTENTIAL.
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2331 MW; F22B51A673023CC9 CRC64;

Query Match 26.0%; Score 13; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
DB 5 PN 6

RESULT 10
RL21_HALCU STANDARD; PRT; 21 AA.
ID RL21_HALCU
AC P05974;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L21e (HL31) (HL30) (Fragment).
GN RPL21E.
OS Halobacterium cutribrium.
OC Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=2242;
RN [1]
RP SEQUENCE.
RX MEDLINE=84282108; PubMed=6467081;
RA Matheson A.T., Yaguchi M., Christensen P., Rollin C.F., Hasnain S.;
RT "Purification, properties, and N-terminal amino acid sequence of
RT certain 50S ribosomal subunit proteins from the archaeobacterium

RT Halobacterium cutirubrum";
 RL Can. J. Biochem. Cell Biol. 62:426-433(1984).
 CC -1- SIMILARITY: BELONGS TO THE L21E FAMILY OF RIBOSOMAL PROTEINS.
 DR PIR; S08558; S08558.
 DR InterPro; IPR001147; Ribosomal L21e.
 DR PROSITE; PS01171; RIBOSOMAL_L21E; PARTIAL.
 KW Ribosomal protein.
 FT NON TER 21
 SQ SEQUENCE 21 AA; 2223 MW; 285A9D10CEDFD7EB CRC64;

Query Match
 Best Local Similarity 26.0%; Score 13; DB 1; Length 21;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 ||
 DB 1 PN 2

RESULT 11
 ID YFLA_METVO STANDARD; PRT; 21 AA.
 AC P42017;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein in FLAB3 3'region (Fragment).
 OS Methanococcus voltae.
 CC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 CC Methanococcaceae; Methanococcus.
 OC NCBI_TaxID=2188;
 RN SEQUENCE FROM N.A.
 RP STRAIN=DSM 1537 / PS;
 RX MEDLINE=92041608; PubMed=1718944;
 RA Kaimakoff M.L., Jarrell K.F.;
 RT "Cloning and sequencing of a multigene family encoding the flagellins
 RT of Methanococcus voltae.";
 RL J. Bacteriol. 173:7113-7125(1991).

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CC -----
 CC EMBL; M72148; -; NOT_ANNOTATED_CDS.
 DR PIR; E41316; E41316.
 KW Hypothetical protein.
 FT NON TER 21
 SQ SEQUENCE 21 AA; 2404 MW; 1FA9CC772365C2DC CRC64;

Query Match
 Best Local Similarity 100.0%; Score 13; DB 1; Length 21;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 ||
 DB 2 PN 3

RESULT 12
 ID PSBH_SYNNU STANDARD; PRT; 20 AA.
 AC P19052;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Photosystem II 10 kDa phosphoprotein (Fragment).
 GN PSBH.
 OS Synechococcus vulcanus (Thermosynechococcus vulcanus).

OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 ON NCBI_TaxID=32053;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=89153587; PubMed=2493396;
 RA Koike H., Manada K., Ikeuchi M., Inoue Y.;
 RT "Low-molecular-mass proteins in cyanobacterial photosystem II:
 RT identification of psbH and psbK gene products by N-terminal
 RT sequencing.";
 RL FEBS Lett. 244:391-396(1989).
 CC -1- SIMILARITY: BELONGS TO THE PSBH FAMILY.
 DR PIR; S03335; S03335.
 DR InterPro; IPR01056; PSII_PsbH.
 DR Pfam; PF00737; PsbH; 1.
 KW Photosystem II; Phosphorylation.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2345 MW; 8CAAB907C5767178 CRC64;

Query Match
 Best Local Similarity 24.0%; Score 12; DB 1; Length 20;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NXXY 5
 ||
 DB 14 NSEY 17

RESULT 13
 ID SODM_HORVU STANDARD; PRT; 20 AA.
 AC P28524;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1) (Fragment).
 GN SODA.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Hordeum.
 ON NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE.
 RP STRAIN=cv. CM 72; TISSUE=Root;
 RA Huxman W.J., Tao H.P., Tanaka C.K.;
 RT "Germin-like polypeptides increase in barley roots during salt
 RT stress.";
 RL Plant Physiol. 97:366-374(1991).
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Manganese (By similarity).
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.

DR InterPro; IPR001189; SODdismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR PROSITE; PS00088; SOD_MN; PARTIAL.
 KW Oxidoreductase; Manganese; Mitochondrion.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2152 MW; 7F7CA8BDF1C9657 CRC64;

Query Match
 Best Local Similarity 24.0%; Score 12; DB 1; Length 20;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
 ||
 DB 7 PDLRY 11

RESULT 14

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HPAA_STRGD
ID HPAA_STRGD STANDARD; PRT; 21 AA.
AC P80437;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Hydroxyphicolinic acid activating enzyme (Fragment).
OS Streptomyces griseoviridis.
OC Bacteria; Actinobacteria; Actinobacteriales (class); Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=45398;
RN [1]
RN SEQUENCE.
RA Pahl A., Schlumbohm W., Keller U.;
RL Submitted (MAR-1995) to the SWISS-PROT data bank.
CC -!- FUNCTION: INVOLVED IN ETAMYCIN BIOSYNTHESIS.
KW Antibiotic biosynthesis.
FT NON TER 21
SQ SEQUENCE 21 AA; 2312 MW; 61F19D160FEDBE4A CRC64;

Query Match 24.0%; Score 12; DB 1; Length 21;
Best Local Similarity 33.3%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 YXXXXY 16
DB 16 YYAAGY 21

RESULT 15
TL19_ARATH STANDARD; PRT; 21 AA.
ID TL19_ARATH
AC P82658;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thylakoid lumenal 19 kDa protein (P19) (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE.
RC STRAIN=cv. Columbia;
RA Kieselbach T., Bystedt M., Schroeder W.P.;
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
KW Chloroplast; Thylakoid.
FT NON TER 21
SQ SEQUENCE 21 AA; 2199 MW; EAA1345E72C00054 CRC64;

Query Match 24.0%; Score 12; DB 1; Length 21;
Best Local Similarity 50.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NXXY 5
DB 3 NQTY 6

RESULT 16
CAT4_FASHE STANDARD; PRT; 20 AA.
ID CAT4_FASHE
AC P80528;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cathepsin L-like cysteine proteinase (EC 3.4.22.-) (Newly excysted
DE juvenile protein 4) (Fragment).
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomata; Fasciolidae; Fasciola.

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OX NCBI_TaxID=6192;
RN [1]
RN SEQUENCE.
RX MEDLINE=95366993; PubMed=7639732;
RA Tkalcic J., Ashman K., Meusen E.;
RT "Fasciola hepatica: rapid identification of newly excysted juvenile
RT proteins."
RL Biochem. Biophys. Res. Commun. 213:169-174(1995).
CC -!- FUNCTION: THIOL PROTEASE.
CC -!- SUBCELLULAR LOCATION: Lysosomal (Potential).
CC -!- DEVELOPMENTAL STAGE: EXPRESSED AT THE NEWLY EXCYSTED JUVENILE
CC STAGE.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
DR MEROPS; C01.033;
DR Interpro: IPR000169; SHprot acsite.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; PARTIAL.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; PARTIAL.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; PARTIAL.
KW Hydrolyase; Thiol protease; Lysosome.
FT NON TER 20
SQ SEQUENCE 20 AA; 2515 MW; D6F75BCA63C91FD6 CRC64;

Query Match 22.0%; Score 11; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 5.3e+03;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NXXY 5
DB 14 NKEY 17

RESULT 17
FIBR_PACLE STANDARD; PRT; 20 AA.
ID FIBR_PACLE
AC P81070;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Fibrinogen (VHDL) (Fragment).
OS Pacifastacus leniusculus (Signal crayfish).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC Astacidea; Astacoidae; Astacidae; Pacifastacus.
OX NCBI_TaxID=6720;
RN [1]
RN SEQUENCE.
RX MEDLINE=96074573; PubMed=7488215;
RA Hall M., van Heusden M.C., Soederhaell K.;
RT "Identification of the major lipoproteins in crayfish hemolymph as
RT proteins involved in immune recognition and clotting."
RL Biochem. Biophys. Res. Commun. 216:939-946(1995).
CC -!- FUNCTION: INVOLVED IN LIPID TRANSPORT. PLAYS A ROLE IN HEMOLYMPH
CC CLOTTING. MAY BE INVOLVED IN WOUND HEALING IN THE CUTICLE.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: SECRETED INTO THE HEMOLYMPH.
CC -!- SIMILARITY: TO VITELLOGENINS.
KW Glycoprotein; Lipid-binding; Hemolymph clotting.
FT NON TER 20
SQ SEQUENCE 20 AA; 2311 MW; 1C04BC596E99FC47 CRC64;

Query Match 22.0%; Score 11; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 5.3e+03;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NXXY 5
DB 4 NLEY 7

RESULT 18
PYRR_PYRAP STANDARD; PRT; 20 AA.
ID PYRR_PYRAP
AC P37362; P80307;

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DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Pyrrhocoricin.
 OS Pyrrhocoris apterus (Sap sucking bug).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
 OC Heteroptera; Pentatomorpha; Lygaeoidea;
 OC Pyrrhocoridae; Pyrrhocoris.
 OC NCBI_TaxID=37000;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RX MEDLINE=94271176; PubMed=8002963;
 RA Cocciandich S., Dupont A., Hegy G., Lanot R., Holder F., Hetru C.,
 RA Hoffmann J.A., Bulet P.;
 RT "Novel inducible antibacterial peptides from a hemipteran insect, the
 sap-sucking bug *Pyrrhocoris apterus*.";
 RL Biochem. J. 300:567-575(1994).
 RN [2]
 RP CARBOHYDRATE-LINKAGE SITE THR-11.
 RX MEDLINE=99177428; PubMed=10076062;
 RA Hoffmann R., Bulet P., Urge L., Ocvos L. Jr.;
 RT "Range of activity and metabolic stability of synthetic antibacterial
 glycopeptides from insects.";
 RL Biochim. Biophys. Acta 1426:459-467(1999).
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE. AFFECTS GRAM-NEGATIVE BACTERIA
 E. COLI 1106, P. AERUGINOSA, E. COLI D22 AND S. CLOACAE AND
 CC -1- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAc DISACCHARIDE, O-
 GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
 CC -1- SIMILARITY: TO DROSOPHILA DROSOCIN.
 DR PIR, S44465; S44465.
 KW Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
 FT CARBOHYD 11 O-LINKED (GALNAc.).
 SQ SEQUENCE 20 AA; 2341 MW; F4320EC2FF29462C CRC64;
 Query Match 22.0%; Score 11; DB 1; Length 20;
 Best Local Similarity 40.0%; Pred. No. 5.3e+03;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 PNXXY 5
 DB 13 PRPIY 17
 RESULT 19
 SC18_MESMA STANDARD; PRT; 20 AA.
 ID SC18_MESMA
 AC P58570;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neurotoxin Bmk 18(2) (Fragment).
 OS Mesobuthus mactensii (Manchurian scorpion) (Butkus mactensii).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Buthoidea; Buthidae; Mesobuthus.
 OC NCBI_TaxID=34649;
 RN [1]
 RP SEQUENCE, AND CHARACTERIZATION.
 RC TISSUE=Venom;
 RX MEDLINE=21383543; PubMed=11491460;
 RA Hahn R., Chen Z., Reddy G., Li Y.;
 RT "Isolation, purification and N-terminal sequencing of a bioactive
 peptide that alters action potentials from the venom of *Butkus
 mactensii* Karach.";
 RL J. Nat. Toxins 10:199-212(2001).
 CC -1- FUNCTION: BINDS TO SODIUM CHANNELS AND INHIBITS THE INACTIVATION
 OF THE ACTIVATED CHANNELS, THEREBY BLOCKING NEURONAL TRANSMISSION.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
 KW ALPHA-TOXIN SUBFAMILY.
 KW Neurotoxin; Sodium channel inhibitor.

FT NON TER 20 20
 SQ SEQUENCE 20 AA; 2349 MW; ED8707568FD0A421 CRC64;
 Query Match 22.0%; Score 11; DB 1; Length 20;
 Best Local Similarity 33.3%; Pred. No. 5.3e+03;
 Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 11 YXXXXY 16
 DB 5 YIAEDY 10
 RESULT 20
 C15Y_STRHY STANDARD; PRT; 20 AA.
 ID C15Y_STRHY
 AC P20903;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Citrate synthase (EC 4.1.3.7) (Fragment).
 GN GLTA.
 OS Streptomyces hygroscopicus.
 OC Bacteria; Actinobacteriia; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OC NCBI_TaxID=1912;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=SF1293;
 RX MEDLINE=90334852; PubMed=1368511;
 RA Shimotohno K.W., Imai S., Murakami T., Seto H.;
 RT "Purification and characterization of citrate synthase from
 Streptomyces hygroscopicus SF-1293 and comparison of its properties
 with those of 2-phosphoenolpyruvate-dependent citrate synthase.";
 RL Agric. Biol. Chem. 54:463-470(1990)
 CC -1- CATALYTIC ACTIVITY: Citrate + CoA = acetyl-CoA + H(2)O +
 oxaloacetate.
 CC -1- ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY NADH.
 CC -1- PATHWAY: Tricarboxylic acid cycle.
 CC -1- SUBUNIT: HOMOHexamers.
 CC -1- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS
 CAPABLE OF OXIDATIVE METABOLISM.
 CC -1- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
 DR PIR, P00046; P00046.
 DR InterPro: IPR002020; Citrate synt.
 DR PROSITE: PS00480; CITRATE SYNTHASE; PARTIAL.
 KW Lyase; Tricarboxylic acid cycle; Allosteric enzyme.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2234 MW; C527ECTA87119597 CRC64;
 Query Match 20.0%; Score 10; DB 1; Length 20;
 Best Local Similarity 33.3%; Pred. No. 9.3e+03;
 Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 11 YXXXXY 16
 DB 9 YGDGEY 14
 RESULT 21
 MCRG_METTE STANDARD; PRT; 20 AA.
 ID MCRG_METTE
 AC P22950;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Methyl-coenzyme M methylreductase gamma subunit (EC 1.8.-.-)
 OS Methanococcus thermophilus.
 OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OC NCBI_TaxID=2210;
 RN [1]
 RP SEQUENCE.

RC STRAIN=DSM 1825 / TM-1;
 RX MEDLINE=91193204; PubMed=2013570;
 RA Jablonski P.E., Ferry J.G.;
 RT "Purification and properties of methyl coenzyme M methylreductase
 from acetate-grown *Methanosarcina thermophila*.";
 RL J. Bacteriol. 173:2481-2487(1991).
 CC -1- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio)
 ethanesulfonic acid) with 7-mercaptoheptanoylthioneine phosphate
 to methane and an heterodisulfide.
 CC -1- CATALYTIC ACTIVITY: CH(3)-S-COM + H-S-HTP = CH(4) + COM-S-S-HTP.
 CC -1- COFACTOR: THE ENZYME COMPLEX BINDS TIGHTLY (BUT NOT COVALENTLY)
 CC TO TWO MOLECULES OF COENZYME F430. F430 IS A YELLOW NICKEL
 PORPHINOID.
 CC -1- PATHWAY: Methanogenesis; last step.
 CC -1- SUBUNIT: TRIMER OF AN ALPHA, A BETA, AND A GAMMA SUBUNIT.
 CC -1- MISCELLANEOUS: THE OPTIMAL TEMPERATURE FOR ENZYME ACTIVITY IS 60
 DEGREES CELSIUS.
 CC -1- MISCELLANEOUS: REDUCED FERREDOXIN COULD REDUCTIVELY REACTIVATE THE
 ENZYME.
 CC InterPro: IPR003178; MCR_gamma.
 DR Pfam: PF02240; MCR_gamma.1.
 KW Methanogenesis; Oxidoreductase.
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2224 MW; DIAACAAAD653658 CRC64;
 Query Match 20.0%; Score 10; DB 1; Length 20;
 Best Local Similarity 33.3%; Pred. No. 9.3e+03;
 Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 11 YXXXXY 16
 DB 2 YEROFY 7
 RESULT 22
 ID SAMP_PLEPL STANDARD; PRT; 20 AA.
 AC P20677;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serum amyloid P-component (SAP) (Fragment).
 OS Pleurocetes platessa (Plaice).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
 OC Pleuronectoidae; Pleuronectidae; Pleuronectes.
 NC NCB1_TaxID=8262;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=82232106; PubMed=7093286;
 RA Pepps W.B., de Beer F.C., Maltstein C.P., March J.F., Feinstein A.,
 RA Butters N., Clamp J.R., Taylor J., Bruton C., Fletcher T.C.;
 RT "C-reactive protein and serum amyloid P component in the plaice
 (*Pleuronectes platessa* L.), a marine teleost, are homologous with
 their human counterparts.";
 RL Blochim. Biophys. Acta 704:123-133(1982).
 CC -1- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
 CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
 CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
 CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
 CC PIR: A05332; A05332.
 DR InterPro: IPR001759; Pentaxin.
 DR PROSITE: PS00289; PENTAXIN; PARTIAL.
 KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
 FT DOMAIN 1 >20
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2292 MW; B94BBB1467BBD75D CRC64;
 Query Match 20.0%; Score 10; DB 1; Length 20;
 Best Local Similarity 50.0%; Pred. No. 9.3e+03;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
 DB 18 PB 19
 RESULT 23
 ID FA71_TETPY STANDARD; PRT; 21 AA.
 AC P81424;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 71 kDa F-actin binding protein (Fragment).
 OS Tetrahymena pyriformis.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomida;
 OC Tetrahymenida; Tetrahymena.
 NC NCB1_TaxID=5908;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=98207047; PubMed=9538250;
 RA Watanabe A., Kurasaawa Y., Watanabe Y., Numata O.;
 RT "A new Tetrahymena actin-binding protein is localized in the division
 furrow.";
 RL J. Biochem. 123:607-613(1998).
 CC -1- FUNCTION: BINDS DIRECTLY TO F-ACTIN AND INDUCES ACTIN FILAMENT
 CC BUNDLING. MAY FUNCTION AS A REGULATOR OF ACTIN FILAMENT
 CC ORGANIZATION.
 CC -1- DEVELOPMENTAL STAGE: CO-LOCALIZED WITH ACTIN IN THE ORAL APPARATUS
 CC IN INTERPHASE CELLS. IN DIVIDING CELLS CO-LOCALIZED WITH ACTIN IN
 CC THE DIVISION FURROW.
 CC -1- PTM: THE N-TERMINUS IS BLOCKED.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
 CC 7.5. ITS MW IS: 71 kDa.
 CC -1- SIMILARITY: TO YEAST FIMBRIN.
 KW Actin-binding.
 FT NON_TER 21 21
 SQ SEQUENCE 21 AA; 2691 MW; 104FD6F5B08FD28 CRC64;
 Query Match 20.0%; Score 10; DB 1; Length 21;
 Best Local Similarity 50.0%; Pred. No. 9.7e+03;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 NXXY 5
 DB 9 NHPY 12
 RESULT 24
 ID LE04_BIOGL STANDARD; PRT; 21 AA.
 AC P80743;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemolymph 65 kDa lectin BG04 (Fragment).
 GN BG04.
 OS Biomphalaria glabrata (Bloodfluke planorb).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 OC Planorbidae; Biomphalaria.
 NC NCB1_TaxID=6526;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=M-LINE; TISSUE=Hemolymph;
 RX MEDLINE=97385165; PubMed=9238039;
 RA Adema C.M., Hertel L.A., Miller R.D., Loker E.S.;
 RT "A family of fibrinogen-related proteins that precipitates parasite-
 derived molecules is produced by an invertebrate after infection.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:8691-8696(1997).
 CC -1- FUNCTION: BINDS AND PRECIPITATES ANTIGENS OF THE PARASITE
 CC ECHINOSTOMA PARANSETI.
 CC -1- SUBCELLULAR LOCATION: SECRETED IN THE HEMOLYMPH.
 CC -1- INDUCTION: BY INFECTION.

KW Lectin.
 FT NON_TER 1
 RT NON_TER 21
 SQ SEQUENCE 21 AA; 2239 MW; B8593D7A4902858C CRC64;

Query Match 20.0%; Score 10; DB 1; Length 21;
 Best Local Similarity 20.0%; Pred. No. 9.7e+03;
 Matches 1; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
 | :
 Db 3 PDCAF 7

RESULT 25
 SODF_PASPI STANDARD; PRT; 20 AA.
 AC P81527;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
 GN SODB.
 OS Pasteurella piscicida (Photobacterium damsela (subsp. piscicida)).
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae;
 CC Photobacterium.
 CX NCBI_TaxId=38294;
 RN [1]
 RP SEQUENCE.

RC STRAIN=MT1415;
 RA MEDLINE=99173752; PubMed=10075430;
 RA Barnes A.C., Balebona M.C., Horne M.T., Ellis A.E.;
 RT "Superoxide dismutase and catalase in Photobacterium damsela subsp.
 RT piscicida and their roles in resistance to reactive oxygen species.";
 RL Microbiology 145:483-494(1999).
 CC -1- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -1- COFACTOR: Iron.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 DR InterPro: IPR001189; SODismutase.
 DR Pfam: PF00081; sodfe; 1.
 KW Oxidoreductase; Iron; Periplasmic.
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2153 MW; A8D31FDAE8553B6D CRC64;

Query Match 18.0%; Score 9; DB 1; Length 20;
 Best Local Similarity 40.0%; Pred. No. 1.6e+04;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PNXXY 5
 | :
 Db 5 PALPY 9

RESULT 26
 YQAH_KLEAE STANDARD; PRT; 20 AA.
 AC P56506;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein YQAH (Fragment).
 GN YQAH.
 OS Klebsiella aerogenes.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Klebsiella.
 CX NCBI_TaxId=28451;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=89056707; PubMed=3057324;
 RA Goncharoff P., Nichols B.P.;
 RT "Evolution of aminobenzoate synthases: nucleotide sequences of
 RT Salmonella typhimurium and Klebsiella aerogenes pabB.";

RL Mol. Biol. Evol. 5:531-548(1988).
 RN [2]
 RP IDENTIFICATION.
 RX MEDLINE=98248213; PubMed=9588799;
 RA Rudd K.E., Humphrey-Smith I., Wasinger V.C., Bairoch A.;
 RT "Low molecular weight proteins: a challenge for post-genomic
 RT research.";

RL Electrophoresis 19:536-544(1996).
 CC -1- SIMILARITY: BELONGS TO THE UPF0181 FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; M22078; -; NOT ANNOTATED_CDS.
 DR InterPro: IPR005371; UPF0181.
 DR Pfam: PF03701; UPF0181; 1.
 KW Hypothetical protein.
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2270 MW; E8AF6425DD9BC88 CRC64;

Query Match 18.0%; Score 9; DB 1; Length 20;
 Best Local Similarity 20.0%; Pred. No. 1.6e+04;
 Matches 1; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
 | :
 Db 6 PLSH 10

RESULT 27
 ACPH_BOVIN STANDARD; PRT; 20 AA.
 AC P80227;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)
 DE (Aph) (Acylaminoacyl-peptidase) (Fragment).
 GN APEH.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 CX NCBI_TaxId=9913;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Lens;
 RX MEDLINE=93387316; PubMed=8375399;
 RA Sharma K.K., Ortwerth B.J.;
 RT "Bovine lens acylpeptide hydrolase. Purification and characterization
 RT of a tetrameric enzyme resistant to urea denaturation and proteolytic
 RT inactivation.";
 RL Eur. J. Biochem. 216:631-637(1993).
 CC -1- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
 CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
 CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
 CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
 CC -1- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
 CC + peptide.
 CC -1- SUBUNIT: HOMOTETRAMER.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
 CC PIR: S36842; S36842.
 DR InterPro: IPR002471; ProL_endopep_ser.
 DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.

KW Hydrolase. 1 1
 FT NON TER 20 20
 SQ SEQUENCE 20 AA; 2325 MW; B9D028BA8378F624 CRC64;

Query Match 16.0%; Score 8; DB 1; Length 20;
 Best Local Similarity 50.0%; Pred. No. 2.6e+04;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
 Db 2 PD 3

RESULT 28
 BUBB_NARPS STANDARD; PRT; 20 AA.
 ID BUBB_NARPS
 AC P80554;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Bulb protein (Fragment).
 OS Narcissus pseudonarcissus (Daffodil).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
 OC Narcissus.
 OC NCBI_TaxID=39639;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. Golden Harvest; TISSUE=Bulb;
 RA Partis M.D., Barker P., Thomas B.;
 RL Submitted (FEB-1996) to the SWISS-PROT data bank.
 FT UNSURE 2 2 OR N.
 FT NON TER 20 20
 SQ SEQUENCE 20 AA; 2077 MW; 76212FF3A468AD38 CRC64;

Query Match 16.0%; Score 8; DB 1; Length 20;
 Best Local Similarity 50.0%; Pred. No. 2.6e+04;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
 Db 2 PD 3

RESULT 29
 CATI_FASHE STANDARD; PRT; 20 AA.
 ID CATI_FASHE
 AC Q09093;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cathepsin L1 (EC 3.4.22.15) (Fragment).
 OS Fasciola hepatica (Liver Fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 OC Echinostomida; Echinostomata; Fasciolidae; Fasciola.
 OC NCBI_TaxID=6192;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94158959; PubMed=8114809;
 RA Smith A.M., Dowd A.J., McConigle S., Keegan P.S., Brennan G.,
 RA Trudgett A., Dalton J.P.;
 RT Purification of a cathepsin L-like proteinase secreted by adult
 RT Fasciola hepatica.";
 RL Mol. Biochem. Parasitol. 62:1-8(1993).
 CC -1- FUNCTION: THIOL PROTEASE THAT ASSISTS THE PARASITE IN BURROWING
 CC THROUGH THE GUT WALL AND LIVER OF ITS MAMMALIAN HOST.
 CC -1- CATALYTIC ACTIVITY: Specificity close to that of papain. As
 CC compared to cathepsin B, cathepsin L exhibits higher activity
 CC towards protein substrates, but has little activity on Z-Arg-Arg-
 CC NHMe, and no pepidyl-dipeptidase activity.
 CC -1- SUBUNIT: DIMER OF A HEAVY AND A LIGHT CHAIN LINKED BY DISULFIDE
 CC BONDS.

CC -1- SUBCELLULAR LOCATION: Lysosomal.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.

DR MEROPS: C01.033; -;
 DR InterPro: IPR000668; Peptidase_C1.
 DR InterPro: IPR00112; SHProt_acite.
 DR Pfam: PF00112; Peptidase_C1; 1.
 DR PROSITE: PS00139; THIOL_PROTEASE_CYS; PARTIAL.
 DR PROSITE: PS00639; THIOL_PROTEASE_HIS; PARTIAL.
 DR PROSITE: PS00640; THIOL_PROTEASE_ASN; PARTIAL.
 KW Hydrolase; Thiol protease; Lysosome.
 FT NON TER 20 20
 SQ SEQUENCE 20 AA; 2174 MW; 97CDEDB33055BCAE CRC64;

Query Match 16.0%; Score 8; DB 1; Length 20;
 Best Local Similarity 50.0%; Pred. No. 2.6e+04;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
 Db 3 PD 4

RESULT 30
 CHP_THICU STANDARD; PRT; 20 AA.
 ID CHP_THICU
 AC P80486;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Chemotherotroph-specific protein (Fragment).
 OS Thibacillus cuprinus.
 OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Thiomonas.
 OC NCBI_TaxID=36860;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=DSM 5494;
 RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
 RL Submitted (SEP-1995) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
 CC CHEMOTHEROTROPHICALLY.
 FT NON TER 20 20
 SQ SEQUENCE 20 AA; 2167 MW; B5BAEC1BA3238A0A CRC64;

Query Match 16.0%; Score 8; DB 1; Length 20;
 Best Local Similarity 50.0%; Pred. No. 2.6e+04;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
 Db 18 PD 19

RESULT 31
 COGI_CHIOP STANDARD; PRT; 20 AA.
 ID COGI_CHIOP
 AC P34153;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Collagenolytic protease 25 kDa II/III (EC 3.4.21.32) (Fragment).
 OS Chionoecetes opilio (Crab-beetle).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Brachyura; Eubrachyura; Majoidae; Majidae; Chionoecetes.
 OC NCBI_TaxID=41210;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hepatopancreas;
 RX MEDLINE=92120073; PubMed=1663026;
 RA Klimova O.A., Vedishcheva Y.V., Strongin A.Y.;
 RT Isolation and characteristics of collagenolytic enzymes from the
 RT hepatopancreas of the crab Chionoecetes opilio.";
 RT Dokl. Akad. Nauk SSSR 317:482-484(1991).

CC -!- FUNCTION: THIS ENZYME IS A SERINE PROTEASE CAPABLE OF DEGRADING
 CC THE NATIVE TRIPLE HELIX OF COLLAGEN.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins, with broad specificity
 CC for peptide bonds. Degrades native collagen at about 75% of the
 CC length of the molecule from the N-terminus. Low activity on small
 CC molecule substrates of both trypsin and chymotrypsin.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC MEROPS: S01.122; -!
 DR InterPro: IPR001254; Ser protease TRY.
 DR PROSITE: PS00240; TRYPSIN_DOM; PARTIAL.
 DR PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
 DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
 KM Hydroxylase, Serine protease; Collagen degradation.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2204 MW; CE0D7B996E7281A7 CRC64;
 QY Query Match 16.0%; Score 8; DB 1; Length 20;
 Db Best Local Similarity 50.0%; Pred. No. 2.6e+04;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 1 PN 2
 9 PH 10
 RESULT 32
 COXM_THUOB STANDARD; PRT; 20 AA.
 AC P80981;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Cytochrome c oxidase polypeptide VIIb-liver (EC 1.9.3.1) (Fragment).
 OS Thunnus obesus (Bigeye tuna).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
 CC Scombridae; Thunnus.
 OX NCBI_TaxID=8241;
 RN [1]
 RP TISSUE=Liver;
 RC MEDLINE=97454291; PubMed=9310366;
 RX Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 RT liver".
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 KM Oxidoreductase; Mitochondrion.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2213 MW; 03B902A70F3E41A6 CRC64;
 QY Query Match 16.0%; Score 8; DB 1; Length 20;
 Db Best Local Similarity 25.0%; Pred. No. 2.6e+04;
 Matches 1; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 2 NXXY 5
 2 NTSH 5
 RESULT 33
 COXM_THUOB STANDARD; PRT; 20 AA.
 AC P80980;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Cytochrome c oxidase polypeptide VIIb-liver (EC 1.9.3.1) (Fragment).
 OS Thunnus obesus (Bigeye tuna).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
 CC Scombridae; Thunnus.
 OX NCBI_TaxID=8241;
 RN [1]
 RP TISSUE=Heart;
 RC MEDLINE=97454291; PubMed=9310366;
 RX Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 RT liver".
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 KM Oxidoreductase; Mitochondrion.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2204 MW; CE0D7B996E7281A7 CRC64;

DE Cytochrome c oxidase polypeptide VIIb-heart (EC 1.9.3.1) (Fragment).
 OS Thunnus obesus (Bigeye tuna).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
 CC Scombridae; Thunnus.
 OX NCBI_TaxID=8241;
 RN [1]
 RP TISSUE=Heart;
 RC MEDLINE=97454291; PubMed=9310366;
 RX Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 RT liver".
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 KM Oxidoreductase; Mitochondrion.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2303 MW; 0A33BD3406E5AA6 CRC64;
 QY Query Match 16.0%; Score 8; DB 1; Length 20;
 Db Best Local Similarity 25.0%; Pred. No. 2.6e+04;
 Matches 1; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 2 NXXY 5
 2 NTSH 5
 RESULT 34
 CP35_PAPSP STANDARD; PRT; 20 AA.
 AC P80056;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DE Cytochrome P450 3A5 (EC 1.14.14.1) (CYP11A5) (P450 3A) (6-beta-
 DE testosterone hydroxylase) (Fragment).
 OS Papio sp. (Baboon).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecinae; Papio.
 OX NCBI_TaxID=61183;
 RN [1]
 RP TISSUE=Liver;
 RC MEDLINE=92174920; PubMed=1541278;
 RX Dalet-Beluche I., Boulenc X., Fabre G., Maurer P., Bonfils C.,
 RA "Purification of two Cytochrome P450 isoforms related to CYP2A and
 RT CYP3A gene families from monkey (baboon, Papio papio) liver
 RT microsomes. Cross reactivity with human forms".
 RL Eur. J. Biochem. 204:641-648(1992).
 CC -!- FUNCTION: 6-BETA-TESTOSTERONE HYDROXYLASE.
 CC -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
 CC oxidized flavoprotein + H(2)O.
 CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR PIR, S21176; S21176.
 DR InterPro: IPR001128; Cytochrome_P450.
 DR PROSITE: PS00086; CYTOCHROME_P450; PARTIAL.
 KM Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 KM Microsome; Endoplasmic reticulum.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2226 MW; 3FEF8B6E62BC0F36 CRC64;
 QY Query Match 16.0%; Score 8; DB 1; Length 20;
 Db Best Local Similarity 50.0%; Pred. No. 2.6e+04;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
1
5 PD 6

Db 5 PD 6

RESULT 35
FIBR_ELEMA
ID FIBR_ELEMA STANDARD; PRT; 20 AA.
AC P14538;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Elephas maximus (Indian elephant).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Proboscidea; Elephantidae; Elephas.
OX NCBI_TaxID=9783;
RN [1]
RP SEQUENCE.
RA O'Neil P.B., Doolittle R.F.;
RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL Syst. Zool. 22:590-595(1973).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR InterPro: IPR002181; Fibrinogen.C.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation.
FT PEPTIDE 1 20 FIBRINOPEPTIDE B.
FT MOD_RES 4 4 SULFATION.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2107 MW; B4F52B959933273 CRC64;

Query Match 16.0%; Score 8; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.6e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
1
15 PS 16

Db 15 PS 16

RESULT 36
HELT_HELHO
ID HELT_HELHO STANDARD; PRT; 20 AA.
AC P46693;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Helohermine (Fragment).
OS Heloderma horridum horridum (Mexican beaded lizard).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosaurs; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;
OC Heloderma.
OX NCBI_TaxID=8552;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90260878; PubMed=1693019;
RA Mocha-Morales J., Martin B.M., Possant L.D.;
RT "Isolation and characterization of helohermine, a novel toxin from
Heloderma horridum horridum (Mexican beaded lizard) venom.";
RL Toxinon 28:299-309(1990).
CC -1- FUNCTION: TOXIC TO MICE; INDUCES LETHARGY, PARTIAL PARALYSIS OF

CC REAR LIMBS AND LOWERING OF BODY TEMPERATURE, SUGGESTING THAT IT
MIGHT BE A HYPOTHERMIC TOXIN.
CC -1- MISCELLANEOUS: THE COMPLETE PROTEIN HAS AN APPARENT MW OF 25 kDa
AND A PI OF 6.8.
DR PIR; A34859; A34859.
KW Toxin.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2156 MW; 91D62B36F7B4F940 CRC64;

Query Match 16.0%; Score 8; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.6e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
1
14 PD 15

Db 14 PD 15

RESULT 37
LPP2_HUMAN
ID LPP2_HUMAN STANDARD; PRT; 20 AA.
AC P56642;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysophospholipase Ht-60 peak 2 (EC 3.1.1.5) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Leukemia;
RX MEDLINE=93111958; PubMed=1471998;
RA Garavito D., Holsberg F., Steiner M.R., Egan R.W., Clark M.A.;
RT "Butyric acid-induced differentiation of Ht-60 cells increases the
expression of a single lysophospholipase.";
RL Biochem. J. 288:831-837(1992).
CC -1- FUNCTION: DEGRADATION OF LYOPHOSPHOLIPIDS. MAY PLAY AN IMPORTANT
ROLE IN PROTECTING THESE CELLS FROM THE CYTOLYTIC EFFECTS OF THE
LYOPHOSPHOLIPIDS PRODUCED BY THE ACTIVATION OF PHOSPHOLIPASE A2.
CC -1- CATALYTIC ACTIVITY: 2-lysophosphatidylcholine + H(2)O =
CC glycerophosphocholine + a fatty acid anion.
CC -1- INDUCTION: INCREASED BY DIFFERENTIATION OF THE CELLS.
CC -1- PTM: THE N-TERMINUS IS BLOCKED.
KW Hydrolyase; Lipid degradation.
FT NON_TER 1 1
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2138 MW; 15B38FD23D89567 CRC64;

Query Match 16.0%; Score 8; DB 1; Length 20;
Best Local Similarity 25.0%; Pred. No. 2.6e+04;
Matches 1; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NXXY 5
1
12 NAYF 15

Db 12 NAYF 15

RESULT 38
MIF_PIG
ID MIF_PIG STANDARD; PRT; 20 AA.
AC P80528;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Macrophage migration inhibitory factor (MIF) (phenylpyruvate
tautomerase) (Glycosylation-inhibiting factor) (GIF) (Fragment).
GN MIF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;

RN [1]
 RP SEQUENCE.
 RA Riviere S., Bouet F., Menez A., Galat A.;
 RL Submitted (MAR-1997) to the SWISS-PROT data bank.
 CC -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
 CC ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
 CC HOST DEFENSE. ALSO ACTS AS A PHENYLPIRUVATE TAUTOMERASE (BY
 CC SIMILARITY).
 CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
 DR HSP6, P14174; IGIF.
 DR InterPro: IPR001398; MIF.
 DR Pfam: PF01187; MIF; 1.
 DR PROSITE: PS01158; MIF; PARTIAL.
 DR Isomerase; Macrophage; Inflammatory response; Cytokine.
 FT ACT SITE 1
 FT NON_TER 1
 FT SEQUENCE 20 AA; 2147 MW; 3517AF60F3012A61 CRC64;
 SQ
 Query Match 16.0%; Score 8; DB 1; Length 20;
 Best Local Similarity 50.0%; Pred. No. 2.6e+04;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PN 2
 Db 15 PD 16
 RESULT 39
 NTLI_HELAN
 ID NTLI_HELAN STANDARD; PRT; 20 AA.
 AC P82007;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Nonspecific lipid-transfer protein Ap10 (LTP) (NSLTP) (HA-Ap10)
 DE (Fragment).
 OS Helianthus annuus (Common sunflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; eusteridae II; Asterales; Asteraceae; Asteroideae;
 OC Heliantheae; Helianthus.
 OC NCBI_TaxId=4232;
 OX [1]
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RA Regente M.C., De la Canal L.;
 RT "A sunflower LTP-like protein shows antifungal properties and
 RT interacts with negatively-charged phospholipids.";
 RL Submitted (AUG-1999) to the SWISS-PROT data bank.
 CC -!- FUNCTION: PLANT NONSPECIFIC LIPID-TRANSFER PROTEINS TRANSFER
 CC PHOSPHOLIPIDS AS WELL AS GALACTOLIPIDS ACROSS MEMBRANES. MAY PLAY
 CC A ROLE IN WAX OR CUTIN DEPOSITION IN THE CELL WALLS OF EXPANDING
 CC EPIDERMAL CELLS AND CERTAIN SECRETORY TISSUES. ALSO HAS FUNGICIDE
 CC ACTIVITY AGAINST F. SOLANI.
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: SEED.
 CC -!- SIMILARITY: BELONGS TO THE PLANT LTP FAMILY.
 DR InterPro: IPR000528; Plant_LTP.
 DR InterPro: IPR001768; TRY/AMY1_inhlt.
 DR Pfam: PF00234; TRY_alpha_aml1_1.
 DR PROSITE: PS00597; PLANT LTP; PARTIAL.
 DR Plant defense; Fungicide; Lipid-binding; Transport; Multigene family.
 FT NON_TER 20
 FT SEQUENCE 20 AA; 2167 MW; 929DB3C8866C2114 CRC64;
 SQ
 Query Match 16.0%; Score 8; DB 1; Length 20;
 Best Local Similarity 40.0%; Pred. No. 2.6e+04;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 PNXXY 5
 Db 12 PCLPY 16

RESULT 40
 R1PX_CUCPE
 ID R1PX_CUCPE STANDARD; PRT; 20 AA.
 AC P80750;
 DT 01-NOV-1997 (Rel. 35; Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Ribosome-inactivating protein (rRNA N-glycosidase) (EC 3.2.2.22)
 DE (Fragment).
 OS Cucurbita pepo (Vegetable marrow) (Summer squash).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
 OC NCBI_TaxId=3663;
 OX [1]
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Mesocarp;
 RX MEDLINE=971175025; PubMed=9022685;
 RA Yoshinari S., Yokota S., Sawmoto H., Koresawa S., Tamura M.,
 RA Endo Y.;
 RT "Purification, characterization and subcellular localization of a
 RT type-1 ribosome-inactivating protein from the sarcocarp of Cucurbita
 RT pepo.";
 RT Eur. J. Biochem. 242:585-591(1996).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 DR InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP; 1.
 DR PROSITE: PS00275; SHIGA_RICIN; PARTIAL.
 DR Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin.
 FT NON_TER 20
 FT SEQUENCE 20 AA; 2235 MW; 8E753D217FDEAA6D CRC64;
 SQ
 Query Match 16.0%; Score 8; DB 1; Length 20;
 Best Local Similarity 25.0%; Pred. No. 2.6e+04;
 Matches 1; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 2 NXXY 5
 Db 11 SSSY 14
 RESULT 41
 UCRO_EQUAR
 ID UCRO_EQUAR STANDARD; PRT; 20 AA.
 AC P81247;
 DT 15-JUL-1998 (Rel. 36; Created)
 DT 15-JUL-1998 (Rel. 36; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Ubiquinol-cytochrome c reductase complex ubiquinone-binding protein
 DE QP-C (EC 1.10.2.2) (ubiquinol-cytochrome c reductase complex 8 kDa
 DE protein) (Fragment).
 DE OCR8.
 GN Equisetum arvense (Field horsetail) (Common horsetail).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Equisetophyta; Sphenopsida; Equisetales; Equisetaceae; Equisetum.
 OC NCBI_TaxId=3258;
 OX [1]
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=98250768; PubMed=9582354;
 RA Brumme S., Kruft V., Schmitz U.K., Braun H.P.;
 RT "New insights into the co-evolution of cytochrome c reductase and the
 RT mitochondrial processing peptidase.";
 RL J. Biol. Chem. 273:13143-13149(1998).
 CC -!- FUNCTION: THIS IS A COMPONENT OF THE UBIQUINOL-CYTOCHROME C
 CC REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH
 CC IS PART OF THE MITOCHONDRIAL RESPIRATORY CHAIN. THIS SUBUNIT,
 CC TOGETHER WITH CYTOCHROME B, BINDS TO UBIQUINONE (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: QH(2) + 2 ferricytochrome c = Q + 2

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CC ferrocytochrome c.
CC -1- SUBUNIT: PLANTS BCL COMPLEX CONTAINS 10 SUBUNITS; 3 RESPIRATORY
CC SUBUNITS, 2 CORE PROTEINS AND 5 LOW-MOLECULAR WEIGHT PROTEINS.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE UQCRC/OC8 FAMILY.
CC Mitochondrion; Inner membrane; Electron transport; Respiratory chain;
CC Oxidoreductase.
KM NON TER 20 20
SQ SEQUENCE 20 AA; 2338 MW; 3921B02A1EFC8CE9 CRC64;

Query Match 16.0%; Score 8; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.6e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 16 PH 17

RESULT 42
VR90 BORPE
ID VR90 BORPE STANDARD; PRT; 20 AA.
AC P81549;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Virulence-associated outer membrane protein VIR90 (Fragment).
GN VIR90.
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
OC Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP SEQUENCE.
RC STRAIN=Tohama 1;
RX MEDLINE=99179239; PubMed=10079522;
RA Passerini de Rossi B.N., Friedman L.E., Gonzalez Flecha F.L.,
RA Cascello P.R., Franco M.A., Rossi J.P.F.C.;
RT "Identification of Bordetella pertussis virulence-associated outer
RT membrane proteins."
RL FEMS Microbiol. Lett. 172:9-13(1999).
KM Outer membrane; Virulence.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2116 MW; D24E1CDCA665206C CRC64;

Query Match 16.0%; Score 8; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.6e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 8 PS 9

RESULT 43
VSP1 TRIOK
ID VSP1 TRIOK STANDARD; PRT; 20 AA.
AC P20005;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Okinaxobin I (EC 3.4.21.-) (Fragment).
OS Trimeresurus okinavensis (Hime-habu) (Ovophis okinavensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidossauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Ovophis.
OX NCBI_TaxID=8769;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=91185341; PubMed=1964457;
RA Iwasaki A., Shieh T.-C., Shimohigashi Y., Waki M., Kihara H., Ohno M.;

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RT "Purification and characterization of a coagulant enzyme, okinaxobin
RT I, from the venom of Trimeresurus okinavensis (Himehabu snake) which
RT releases fibrinogen B."
RL J. Biochem 108:822-828(1990).
CC -1- FUNCTION: THROMBIN-LIKE SNAKE VENOM SERINE PROTEASE.
CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-GLY BONDS IN
CC FIBRINOGEN ALPHA CHAINS. CLEAVES FIBRINOGEN ALPHA CHAINS
CC PREFERENTIALLY TO BETA CHAINS.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: EXPRESSED BY VENOM GLAND.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. SNAKE VENOM SUBFAMILY.
DR PIR: PX0042; PX0042.
DR MEROPS: S01.185; -.
DR InterPro: IPR001254; Ser protease Try.
DR PROSITE: PS50240; TRYPSIN_DOM; PARTIAL.
DR PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
KM Hydrolase; Serine protease; Venom.
FT NON TER 1 1
SQ SEQUENCE 20 AA; 2249 MW; 69E9FE62EC53F391 CRC64;

Query Match 16.0%; Score 8; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.6e+04;
Matches 1; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 11 YXXXXY 16
DB 14 FLAALY 19

RESULT 44
ALL7 OLEEU
ID ALL7 OLEEU STANDARD; PRT; 21 AA.
AC P81430;
DT 30-MAY-2000 (Rel. 39, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pollen allergen Ole e 7 (Ole e VII) (Fragment).
OS Olea europaea (Common olive).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Oleaceae; Olea.
OX NCBI_TaxID=4146;
RN [1]
RP SEQUENCE (VARIANTS A AND B), AND MASS SPECTROMETRY.
RC TISSUE=Pollen;
RX MEDLINE=99449676; PubMed=10518824;
RA Tejera M.L., Villalba M., Batanero E., Rodriguez R.;
RT "Identification, isolation, and characterization of Ole e 7, a new
RT allergen of olive tree pollen."
RL J. Allergy Clin. Immunol. 104:797-802(1999).
CC -1- POLYMORPHISM: Many isoforms of the allergen exist due to
CC polymorphism. They can be classified as isoforms of type A (shown
CC here) and isoforms of type B. A microheterogeneity is detected at
CC positions 4 and 11 of isoforms of type A and at positions 4, 5, 10
CC and 11 of isoforms of type B.
CC -1- MISCELLANEOUS: Allergen from olive pollen. Important in
CC Mediterranean countries and California. Its prevalence is related
CC to the geographic area.
KM Allergen; Polymorphism.
FT VARIANT 5 5 S -> G (IN TYPE B).
FT VARIANT 10 10 L -> K (IN TYPE B).
FT VARIANT 18 18 I -> K (IN TYPE B).
FT NON TER 21 21
SQ SEQUENCE 21 AA; 2199 MW; F0E9B99FEB079400 CRC64;

Query Match 16.0%; Score 8; DB 1; Length 21;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2

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DB 2 PS 3

RESULT 45

FEDB_AMYME STANDARD; PRT; 21 AA.

AC P80706; 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Formate ester dehydrogenase, beta chain (EC 1.2.99.-) (FEDB)

OS Amycolatopsis methanolica.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Pseudonocardiales; Pseudonocardaceae;

CC Amycolatopsis.

OK NCBI_TaxID=1814;

RN (1)

RP SEQUENCE.

RC STRAIN=NCIB 11946.

RX MEDLINE=96140591; PubMed=8554333;

RA Kim S.W., Luykx D.M.A.M., de Vries S., Duine J.A.;

RT "A second molycoprotein aldehyde dehydrogenase from Amycolatopsis methanolica NCIB 11946."

RL Arch. Biochem. Biophys. 325:1-7(1996).

CC -i- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA AND A GAMMA CHAIN.

KM Oxidoreductase.

FT NON_TER 21

SQ SEQUENCE 21 AA; 2208 MW; 193F40E0285A03B0 CRC64;

Query Match 16.0%; Score 8; DB 1; Length 21;

Best Local Similarity 50.0%; Pred. No. 2.8e+04;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2

DB 11 PS 12

RESULT 46

GRP WHEAT STANDARD; PRT; 21 AA.

ID GERP_WHEAT 229532;

AC 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Pseudogermmin (Fragment).

OS Triticum aestivum (Wheat).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticaceae; Triticum.

OK NCBI_TaxID=4365;

RN (1)

RP SEQUENCE.

RX MEDLINE=93049354; PubMed=1425703;

RA Lane B.G., Cuning A.C., Fregeau J., Carpita N.C., Hurkman W.J., Bernier F., Dratecka-Kos E., Kennedy T.D.,

RT "Germmin isoforms are discrete temporal markers of wheat development. Pseudogermmin is a uniquely thermostable water-soluble oligomeric protein in ungerminated embryos and like germmin in germinated embryos, it is incorporated into cell walls."

RT Eur. J. Biochem. 209:961-969(1992).

RL -i- FUNCTION: MAY SUBSINE THE ROLE OF GERMIN AT THE LOW WATER POTENTIALS DURING EMBRYOGENESIS.

CC -i- SUBUNIT: HOMOTETRAMER.

CC -i- SUBCELLULAR LOCATION: COMPONENT OF THE WALLS OF THE MATURE, UNGERMINATED EMBRYOS.

CC -i- DEVELOPMENTAL STAGE: ACCUMULATES, MAXIMALLY, BETWEEN 20-25-DAYS POSTANTHESIS, THEN DECLINES APPRECIABLY IN AMOUNT BY 30-DAYS POSTANTHESIS, IN SOLUBLE EXTRACTS OF IMMATURE EMBRYOS.

CC -i- SIMILARITY: BELONGS TO THE GERMIN FAMILY.

DR PIR; S27247; S27247.

DR InterPro; IPR001929; Germmin.

DR PROSITE; PS00725; GERMIN; PARTIAL.

KW Apoplast; Cell wall; Multigene family.

FT NON_TER 21

SQ SEQUENCE 21 AA; 2244 MW; 6B846FD67C07D6AC CRC64;

Query Match 16.0%; Score 8; DB 1; Length 21;

Best Local Similarity 50.0%; Pred. No. 2.8e+04;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2

DB 3 PD 4

RESULT 47

MCT3_MOUSE STANDARD; PRT; 21 AA.

AC P21843; 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Mast cell protease 3 (EC 3.4.21.-) (MCP-3) (Fragment).

GN MCP3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OK NCBI_TaxID=10090;

RN (1)

RP SEQUENCE.

RX MEDLINE=90222202; PubMed=2326280;

RA Reynolds D.S., Stevens R.L., Lane W.S., Carr M.H., Austen K.F., Serafini W.E.;

RT "Different mouse mast cell populations express various combinations of at least six distinct mast cell serine proteases."

RL Proc. Natl. Acad. Sci. U.S.A. 87:3230-3234(1990).

CC -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. GRANZYME SUBFAMILY.

DR PIR; A35646; A35646.

DR MEROPS; S01.140; -.

DR MCD; MGI:96939; MCP3.

DR InterPro; IPR001254; Ser_protease_Try.

DR Pfam; PF00089; trypsin_1.

DR PROSITE; PS50240; TRYPSIN_DOM; PARTIAL.

DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.

DR PROSITE; PS00135; TRYPSIN_SER; PARTIAL.

FT Hydrolase; Serine protease.

FT NON_TER 21

SQ SEQUENCE 21 AA; 2328 MW; 6C840866B9D6FA01 CRC64;

Query Match 16.0%; Score 8; DB 1; Length 21;

Best Local Similarity 50.0%; Pred. No. 2.8e+04;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2

DB 9 PH 10

RESULT 48

NEPH_RAT STANDARD; PRT; 21 AA.

AC P58522; 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Nephritogenesis.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OK NCBI_TaxID=10116;

RN (1)

RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-1.

DR Tissue=Renal glomerulus;

```

RX MEDLINE=88315043; PubMed=3410849;
RA Shibata S., Takeda T., Natori Y.;
RT "The structure of nephritogenoside. A nephritogenic glycopeptide with
RT alpha-N-glycosidic linkage."
RL J. Biol. Chem. 263:12483-12485(1988).
CC -1- FUNCTION: Can induce glomerulonephritis.
CC -1- PTM: N-terminal Asn contains an unusual Glc tri-saccharide. The
CC sugar portion confers the activity to nephritogenoside.
KW Repeat; Glycoprotein.
FT DOMAIN 5 19 5 X 3 AA TANDEM REPEATS OF G-X-X.
FT REPEAT 5 7 1.
FT REPEAT 8 10 2.
FT REPEAT 11 13 3.
FT REPEAT 14 16 4.
FT REPEAT 17 19 5.
FT CARBOHYD 1 1 N-LINKED (GLC...);
SQ SEQUENCE 21 AA; 1983 MW; 62C70D2E0EFC37 CRC64;

Query Match 16.0%; Score 8; DB 1; Length 21;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 15 PS 16

RESULT 49
NRLA ACISP STANDARD; PRT; 21 AA.
ID NRLA ACISP
AC P33036;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Nitrilase (EC 3.5.5.1) (Fragment).
OS Acinetobacter sp. (strain AK226).
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_TaxID=472;
RN [1]
RP SEQUENCE.
RX MEDLINE=91345837; PubMed=1369128;
RA Yamamoto K., Komatsu K.;
RT "Purification and characterization of nitrilase responsible for the
RT enantioselective hydrolysis from Acinetobacter sp. AK 226."
RL Agric. Biol. Chem. 55:1459-1466(1991).
CC -1- FUNCTION: ACTS ON MANY KINDS OF NITRILE COMPOUNDS SUCH AS
CC ALIPHATIC, AROMATIC, AND HETEROCYCLIC MONONITRILES OR DINITRILES.
CC PREFERS S-(+)-2-(4'-ISOBUTYLPHENYL)-PROPIONITRILE TO R-(+)-2-(4'-
CC ISOBUTYLPHENYL)-PROPIONITRILE AS THE SUBSTRATE.
CC -1- CATALYTIC ACTIVITY: A nitrile + H(2)O = a carboxylate + NH(3).
CC -1- SIMILARITY: BELONGS TO THE NITRILASE FAMILY.
DR InterPro; IPR000132; N/CN hydrolase.
DR PROSITE; PS00920; NITRIL_CHT_1; PARTIAL.
DR PROSITE; PS00921; NITRIL_CHT_2; PARTIAL.
KW Hydrolase.
FT NON_TER 21
SQ SEQUENCE 21 AA; 2223 MW; 5FA741C41EAC19B CRC64;

Query Match 16.0%; Score 8; DB 1; Length 21;
Best Local Similarity 25.0%; Pred. No. 2.8e+04;
Matches 1; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NXXY 5
DB 4 NSKF 7

RESULT 50
SCIB_BPTS STANDARD; PRT; 21 AA.
ID SCIB_BPTS
AC P23208;

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DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1991 (Rel. 20, Last annotation update)
DE Scib protein (Fragment).
GN SCIB.
OS Bacteriophage T5.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC T5-like viruses.
OX NCBI_TaxID=10726;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91123205; PubMed=1825083;
RA Krauel V., Heller K.J.;
RT "Cloning, sequencing, and recombinational analysis with bacteriophage
RT B23 of the bacteriophage T5 cad gene encoding the receptor-binding
RT protein."
RL J. Bacteriol. 173:1287-1297(1991).
CC -1- FUNCTION: MAY DETERMINE THE SINGLE-STRAND INTERRUPTIONS IN T5 DNA,
CC TOGETHER WITH THE SCIA GENE PRODUCT.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M62847; AAA32560.1; -
FT NON_TER 21
SQ SEQUENCE 21 AA; 2247 MW; 4C0C7D4E3B76FAAB CRC64;

Query Match 16.0%; Score 8; DB 1; Length 21;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 8 PD 9

```

Search completed: June 11, 2003, 07:42:43
Job time : 16 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 11, 2003, 07:42:19 ; Search time 28 Seconds
(without alignments)
154.535 Million cell updates/sec

Title: US-09-883-727A-127

Perfect score: 50
Sequence: 1 PXXXXXXXXXXXXXXXXXXXX 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1657

Minimum DB seq length: 20
Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 150 summaries

Database :

SPREMBL_21: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriaph: *
17: sp_archaeop: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	30.0	21	2	046419 chlamydia t
2	14	28.0	20	4	09UCB6
3	14	28.0	20	5	09TW15
4	14	28.0	21	11	09RIH1
5	13	26.0	20	2	067962
6	13	26.0	20	2	051950
7	13	26.0	20	2	051952
8	13	26.0	20	2	09F105
9	13	26.0	20	2	09F416
10	13	26.0	20	2	09R4V3
11	13	26.0	20	4	09UCB7
12	13	26.0	20	4	09UCB7
13	13	26.0	20	6	09UCB6
14	13	26.0	20	6	09TTC3
15	13	26.0	20	6	028079
16	13	26.0	20	6	P82666

17	13	26.0	20	8	09SL60	08S160 aecium dec
18	13	26.0	20	10	P82163	P82163 spincia ol
19	13	26.0	20	10	09S8X5	09S8X5 glycine max
20	13	26.0	20	10	09S8R2	09S8R2 solanum tub
21	13	26.0	20	11	09QV62	09QV62 ratus sp.
22	13	26.0	20	11	09QV66	09QV66 ratus sp.
23	13	26.0	20	12	085096	085096 punca toro
24	13	26.0	20	12	084860	084860 unidentified
25	13	26.0	20	12	065710	065710 beane virus
26	13	26.0	20	13	09PRM6	09PRM6 scyllorhinu
27	13	26.0	20	13	09PRU0	09PRU0 gallus gall
28	13	26.0	20	13	09PRR4	09PRR4 scyllorhinu
29	13	26.0	20	13	09PRR3	09PRR3 scyllorhinu
30	13	26.0	20	13	09PRR8	09PRR8 gadus morhu
31	13	26.0	20	15	09DPR0	09DPR0 human immun
32	13	26.0	21	2	09X3D3	09X3D3 prochloroco
33	13	26.0	21	2	09X3E5	09X3E5 prochloroco
34	13	26.0	21	2	09X3G5	09X3G5 prochloroco
35	13	26.0	21	2	09X3H2	09X3H2 prochloroco
36	13	26.0	21	2	09X3J7	09X3J7 prochloroco
37	13	26.0	21	2	09X3K7	09X3K7 prochloroco
38	13	26.0	21	2	044611	044611 buchnera ap
39	13	26.0	21	2	09WM36	09WM36 prochloroco
40	13	26.0	21	2	09R500	09R500 bacillus su
41	13	26.0	21	2	09R4T3	09R4T3 mycobacteri
42	13	26.0	21	2	053014	053014 rhizobium e
43	13	26.0	21	3	09UR89	09UR89 coccidioid
44	13	26.0	21	4	09HD54	09HD54 homo sapien
45	13	26.0	21	4	012812	012812 homo sapien
46	13	26.0	21	4	09UD00	09UD00 homo sapien
47	13	26.0	21	5	061553	061553 dirosophila
48	13	26.0	21	6	09T020	09T020 sus scrofa
49	13	26.0	21	6	09TRP5	09TRP5 bos taurus
50	13	26.0	21	7	08WLR1	08WLR1 homo sapien
51	13	26.0	21	10	09M3S8	09M3S8 arabidopsis
52	13	26.0	21	10	0941R2	0941R2 arabidopsis
53	13	26.0	21	10	09S8L0	09S8L0 cucumis sat
54	13	26.0	21	11	08V1L1	08V1L1 mus musculu
55	13	26.0	21	11	09PS51	09PS51 lampetra fl
56	12	24.0	20	2	047614	047614 escherichia
57	12	24.0	20	2	09R5T5	09R5T5 proteus mir
58	12	24.0	20	2	09R500	09R500 streptomyce
59	12	24.0	20	2	09R498	09R498 pseudomonas
60	12	24.0	20	2	09R4L7	09R4L7 leucosostoc
61	12	24.0	20	4	08WU51	08WU51 homo sapien
62	12	24.0	20	5	09TW18	09TW18 ceratitlis c
63	12	24.0	20	10	P83143	P83143 maiva parvi
64	12	24.0	20	12	065705	065705 bovine resp
65	12	24.0	20	12	08V686	08V686 bovine resp
66	12	24.0	20	13	09PR55	09PR55 oncorhynch
67	12	24.0	21	2	09AJG0	09AJG0 vibrio pala
68	12	24.0	21	10	008934	008934 nicotiana t
69	12	24.0	21	11	063076	063076 ratus norv
70	12	24.0	21	11	09QU020	09QU020 ratus sp.
71	12	24.0	21	12	08V5Y0	08V5Y0 alfalfa mos
72	12	24.0	21	12	083966	083966 influenzavi
73	12	24.0	21	12	084058	084058 influenzavi
74	12	24.0	21	13	0902J3	0902J3 gallus gall
75	12	24.0	21	15	0910Y4	0910Y4 human immun
76	11	22.0	20	2	09R896	09R896 chlamydia t
77	11	22.0	20	2	049448	049448 mycoplasma
78	11	22.0	20	2	046499	046499 desulfovibr
79	11	22.0	20	2	09R4W9	09R4W9 pseudomonas
80	11	22.0	20	2	09R4W0	09R4W0 campylobact
81	11	22.0	20	4	096KZ0	096KZ0 homo sapien
82	11	22.0	20	4	09UC63	09UC63 homo sapien
83	11	22.0	20	6	09TR04	09TR04 bos taurus
84	11	22.0	20	10	09S903	09S903 vigina sinen
85	11	22.0	20	10	09S8Y0	09S8Y0 phleum prat
86	11	22.0	20	11	09ER00	09ER00 mus musculu
87	11	22.0	20	11	099JY2	099JY2 mus musculu
88	11	22.0	20	11	09QV29	09QV29 ratus sp.
89	11	22.0	20	13	09PS14	09PS14 oncorhynch

90	11	22.0	21	2	Q93C14	Q93C14 escherichia
91	11	22.0	21	4	Q9UC55	Q9UC55 homo sapien
92	11	22.0	21	6	Q95JAO	Q95JAO sus scrofa
93	11	22.0	21	8	Q9ZXB7	Q9ZXB7 spinaria sp
94	11	22.0	21	11	Q9RIC3	Q9RIC3 mus musculu
95	11	22.0	21	11	Q9ESX0	Q9ESX0 mus musculu
96	11	22.0	21	11	Q8R488	Q8R488 rattus norv
97	10	20.0	20	4	Q8WV11	Q8WV11 homo sapien
98	10	20.0	20	4	Q9UC62	Q9UC62 homo sapien
99	10	20.0	20	6	Q18764	Q18764 sus scrofa
100	10	20.0	20	6	Q9TR55	Q9TR55 ovis aries
101	10	20.0	20	8	P92689	P92689 podospora a
102	10	20.0	20	8	Q9T2N9	Q9T2N9 gallus gall
103	10	20.0	20	10	P83368	P83368 lupinus lut
104	10	20.0	20	10	P83365	P83365 lupinus lut
105	10	20.0	20	10	P83364	P83364 lupinus lut
106	10	20.0	20	10	P83363	P83363 lupinus lut
107	10	20.0	20	10	Q9S806	Q9S806 triticum ae
108	10	20.0	20	10	Q9S806	Q9S806 lupinus alb
109	10	20.0	20	13	Q9PRM4	Q9PRM4 gallus gall
110	10	20.0	20	16	Q8X9P6	Q8X9P6 escherichia
111	10	20.0	21	2	Q9R4C5	Q9R4C5 agrobacteri
112	10	20.0	21	2	Q9R5E0	Q9R5E0 aeromonas h
113	10	20.0	21	3	Q9UR74	Q9UR74 yarrowia li
114	10	20.0	21	6	Q9SN72	Q9SN72 equus cabal
115	10	20.0	21	8	Q35556	Q35556 pythium oli
116	10	20.0	21	10	Q42732	Q42732 flaveria bi
117	10	20.0	21	10	Q42734	Q42734 flaveria bi
118	9	18.0	20	2	Q53345	Q53345 pseudomonas
119	9	18.0	20	2	Q9R4M4	Q9R4M4 helicobacte
120	9	18.0	20	3	Q9C3Y3	Q9C3Y3 sclerocinia
121	9	18.0	20	3	Q9C3Y2	Q9C3Y2 sclerocinia
122	9	18.0	20	3	Q9C3Y1	Q9C3Y1 sclerocinia
123	9	18.0	20	3	Q9C3Y0	Q9C3Y0 sclerocinia
124	9	18.0	20	3	Q9C3X9	Q9C3X9 sclerocinia
125	9	18.0	20	3	Q9C3X8	Q9C3X8 sclerocinia
126	9	18.0	20	3	Q9C3X7	Q9C3X7 sclerocinia
127	9	18.0	20	3	Q9C3X6	Q9C3X6 sclerocinia
128	9	18.0	20	3	Q9C3X5	Q9C3X5 sclerocinia
129	9	18.0	20	3	Q9C3X4	Q9C3X4 sclerocinia
130	9	18.0	20	3	Q9C3X3	Q9C3X3 sclerocinia
131	9	18.0	20	3	Q9C3X2	Q9C3X2 sclerocinia
132	9	18.0	20	3	Q9C3X1	Q9C3X1 sclerocinia
133	9	18.0	20	3	Q9C3X0	Q9C3X0 sclerocinia
134	9	18.0	20	3	Q9C3W9	Q9C3W9 sclerocinia
135	9	18.0	20	3	Q9C3W8	Q9C3W8 sclerocinia
136	9	18.0	20	3	Q9C3W7	Q9C3W7 sclerocinia
137	9	18.0	20	3	Q9C3W6	Q9C3W6 sclerocinia
138	9	18.0	20	3	Q9C3W5	Q9C3W5 sclerocinia
139	9	18.0	20	3	Q9C3W4	Q9C3W4 sclerocinia
140	9	18.0	20	3	Q9C3W3	Q9C3W3 sclerocinia
141	9	18.0	20	3	Q9C3W2	Q9C3W2 sclerocinia
142	9	18.0	20	3	Q9C3W1	Q9C3W1 sclerocinia
143	9	18.0	20	3	Q9C3W0	Q9C3W0 sclerocinia
144	9	18.0	20	3	Q9C3V9	Q9C3V9 sclerocinia
145	9	18.0	20	3	Q9C3V8	Q9C3V8 sclerocinia
146	9	18.0	20	3	Q9C3V7	Q9C3V7 sclerocinia
147	9	18.0	20	3	Q9C3V6	Q9C3V6 sclerocinia
148	9	18.0	20	3	Q9C3V5	Q9C3V5 sclerocinia
149	9	18.0	20	3	Q9C3V4	Q9C3V4 sclerocinia
150	9	18.0	20	3	Q9C3V3	Q9C3V3 sclerocinia

ALIGNMENTS

RESULT 1

Q46419 PRELIMINARY; PRT; 21 AA.
 AC Q46419; 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)

DE Major outer membrane protein variable domain II (Fragment).
 GN OMP1.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 ON NCB1_TaxID=813;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=D-;
 RX MEDLINE=89173295; PubMed=2466791;
 RA Yuan Y., Zhang Y.-X., Watkins N.G., Caldwell H.D.;
 RT "Nucleotide and Deduced Amino Acid Sequences for the Four Variable
 RT Domains of the Major Outer Membrane Proteins of the 15 Chlamydia
 RT trachomatis Serovars.";
 RL Infect. Immun. 57:1040-1049(1989).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=D-;
 RX MEDLINE=93114875; PubMed=8418043;
 RA Lampe M.F., Suchland R.J., Stamm W.E.;
 RT "Nucleotide sequence of the variable domains within the major outer
 RT membrane protein gene from serovariants of Chlamydia trachomatis.";
 RL Infect. Immun. 61:213-219(1993).
 DR EMBL; L03754; AA859036.1; -.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 21 AA; 2341 MW; B7B28C4B4F729A0B CRC64;

Query Match 30.0%; Score 15; DB 2; Length 21;
 Best Local Similarity 40.0%; Pred. No. 3.7e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
 DB 14 PNMSF 18

RESULT 2

Q9UC66 PRELIMINARY; PRT; 20 AA.
 AC Q9UC66;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-OCT-2001 (T-EMBLrel. 18, Last annotation update)
 DE Alpha-ONE antitrypsin (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCB1_TaxID=9606;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=93312288; PubMed=8323530;
 RA Umekawa T., Kohri K., Anasaki N., Yamate T., Yoshida K., Yamamoto K.,
 RA Suzuki Y., Sinozaki H., Kurita T.;
 RT "Sequencing of a urinary stone protein, identical to alpha-one
 RT antitrypsin, which lacks 22 amino acids.";
 RL Biochem. Biophys. Res. Commun. 193:1049-1053(1993).
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR HSPF; P01009; IOLP.
 DR InterPro; IPR000215; Serpin.
 DR Pfam; PF00079; serpin; 1.
 KW Serpin.
 SQ SEQUENCE 20 AA; 2344 MW; ACE25B3BE5786E9 CRC64;

Query Match 28.0%; Score 14; DB 4; Length 20;
 Best Local Similarity 27.3%; Pred. No. 6.3e+03;
 Matches 3; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 PNXXYXXXXXX 11
 DB 6 PNLAEFAPSLY 16

RESULT 3

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O9TWIS
ID O9TWIS PRELIMINARY; PRT; 20 AA.
AC O9TWIS;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE Major cuticular protein (Fragment).
OS Ceratitis capitata (Mediterranean fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Tephritidae; Tephritidae; Ceratitis.
NCBI_TaxID=7213;
RN (1)
RX MEDLINE=95279142; PubMed=759285;
RA Tsiliras A., Korumantou E., Allen G., Dimitriadis G.;
RT "Partial N-terminal sequences of larval cuticular proteins from the
RT dipteran Ceratitis capitata."
RL Hereditas 122:79-83(1995).
SQ SEQUENCE 20 AA; 2329 MW; C6AB80B44ED70B88 CRC64;

Query Match
Best Local Similarity 28.0%; Score 14; DB 5; Length 20;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
DB 15 PDSIV 19

RESULT 4
O9RIH1 PRELIMINARY; PRT; 21 AA.
ID O9RIH1;
AC O9RIH1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Insulin receptor (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN (1)
RX SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Liu Y., Tam J.W.O.;
RT "Partial sequence of rat insulin receptor gene."
RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF110216; AAD40894.1; -.
DR EMBL; AF110215; AAD40894.1; JOINED.
KW Receptor.
KW NON_TER
FT NON_TER 1 1
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2387 MW; CFFCFD937F77DBA8 CRC64;

Query Match
Best Local Similarity 28.0%; Score 14; DB 11; Length 21;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
DB 9 PSSVY 13

RESULT 5
O67962 PRELIMINARY; PRT; 20 AA.
ID O67962;
AC O67962;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE B6/E complex subunit IV (Fragment).
GN PETD.

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OS Prochlorococcus marinus.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1219;
RN (1)
RX SEQUENCE FROM N.A.
RC STRAIN=CMP1375;
RX MEDLINE=98123172; PubMed=9452521;
RA Urbach E., Scanlan D.J., Distel D.L., Waterbury J.B., Chisholm S.W.;
RT "Rapid diversification of marine picophytoplankton with dissimilar
RT light-harvesting structures inferred from sequences of Prochlorococcus
RT and Synechococcus (Cyanobacteria)."
RL J. Mol. Evol. 46:188-201(1998).
DR EMBL; AF001487; AAC05621.1; -.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2242 MW; C3078A1A3C474FDC CRC64;

Query Match
Best Local Similarity 26.0%; Score 13; DB 2; Length 20;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
DB 7 PN 8

RESULT 6
O51950 PRELIMINARY; PRT; 20 AA.
ID O51950;
AC O51950;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Major outer membrane protein (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
RN (1)
RX SEQUENCE FROM N.A.
RX MEDLINE=98055742; PubMed=9395364;
RA Bobo L.D., Novak N., Munoz B., Hsieh Y.H., Quinn T.C., West S.;
RT "Severe disease in children with trachoma is associated with
RT persistent Chlamydia trachomatis infection."
RL J. Infect. Dis. 176:1524-1530(1997).
DR EMBL; AF015548; AAB95376.1; -.
FT NON_TER 1 1
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2209 MW; D838001675219589 CRC64;

Query Match
Best Local Similarity 26.0%; Score 13; DB 2; Length 20;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
DB 15 PN 16

RESULT 7
O51952 PRELIMINARY; PRT; 20 AA.
ID O51952;
AC O51952;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Outer membrane protein (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
RN (1)
RX SEQUENCE FROM N.A.
RA Bobo L., Novak N.G.;
RT "Severe disease in children with trachoma is associated with

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RT persistent Chlamydia trachomatis infection."
 RL J Infect. Dis. 0:0-0(1998).
 DR EMBL:AF015550; AAB95378.1; -.
 FT NON_TER 1
 SQ SEQUENCE 20 AA; 2223 MW; D818044775219589 CRC64;
 Query Match 26.0%; Score 13; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
 DB 15 PN 16

RESULT 8
 Q9F105 PRELIMINARY; PRT; 20 AA.
 AC Q9F105;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Ribosomal protein L35 (Fragment).
 GN RPMI.
 OS Vibrio mimicus.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=674;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC33653;
 RX MEDLINE=21143364; PubMed=11209061;
 RA Rowe-Magnus D.A., Guerout A.-M., Ploncard P., Dychinco B., Davies J., Mazel D.;
 RT "The evolutionary history of chromosomal super-integrans provides an ancestry for multi-resistant integrons.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:652-657(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC33653;
 RA Dychinco B., Guerout A.-M., Davies J., Mazel D.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF180939; AAG34728.1; -.
 FT NON_TER 1
 SQ SEQUENCE 20 AA; 2142 MW; E0759789A53FE8C CRC64;

Query Match 26.0%; Score 13; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
 DB 1 PN 2

RESULT 9
 Q9R4Y6 PRELIMINARY; PRT; 20 AA.
 AC Q9R4Y6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Major outer membrane protein (Fragment).
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; CFB group; Bacteroidetes; Bacteroidales; Porphyromonadaceae;
 OC Porphyromonas.
 OX NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=94268318; PubMed=8208139;
 RA Kokeguchi S., Miyamoto M., Ohyama H., Hongyo H., Takigawa M., Kurihara H., Murayama Y., Kato K.;
 RT "Biochemical properties of the major outer membrane proteins of

RT Porphyromonas gingivalis."
 RL Microbios 77:247-252(1994).
 SQ SEQUENCE 20 AA; 2150 MW; FD89405CE953DA41 CRC64;
 Query Match 26.0%; Score 13; DB 2; Length 20;
 Best Local Similarity 40.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
 DB 10 PDYHY 14

RESULT 10
 Q9R4V3 PRELIMINARY; PRT; 20 AA.
 AC Q9R4V3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Alkaline lipase (EC 3.1.1.3) (Fragment).
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=95036864; PubMed=7765474;
 RA Kojima Y., Yokoe M., Mase T.;
 RL Biosci. Biotechnol. Biochem. 58:1564-1568(1994).
 DR HSSP; P22088; 3LIP.
 SQ SEQUENCE 20 AA; 2177 MW; 24B539FDD5DBB693 CRC64;

Query Match 26.0%; Score 13; DB 2; Length 20;
 Best Local Similarity 33.3%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 YXXXXY 16
 DB 4 YATTRY 9

RESULT 11
 Q9RSV7 PRELIMINARY; PRT; 20 AA.
 AC Q9RSV7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Ribosomal protein L31 (Fragment).
 OS Pseudomonas mendocina.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=300;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95244309; PubMed=7727274;
 RA Ochi K.;
 RT "Comparative ribosomal protein sequence analyses of a phylogenetically defined genus, Pseudomonas, and its relatives.";
 RL Int. J. Syst. Bacteriol. 45:268-273(1995).
 SQ SEQUENCE 20 AA; 2195 MW; C70684512A72E688 CRC64;

Query Match 26.0%; Score 13; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
 DB 7 PN 8

RESULT 12

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Q9UCB7
ID Q9UCB7 PRELIMINARY; PRT; 20 AA.
AC Q9UCB7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE Insulin receptor beta subunit (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94079885; PubMed=8257688;
RA Kasuya J., Paz I.B., Maddux B.A., Goldfine I.D., Hefta S.A.,
RA Fujita-Yamaguchi Y.;
RT "Characterization of human placental insulin-like growth factor-
RT I/Insulin hybrid receptors by protein microsequencing and
RT purification."
RL Biochemistry 32:13531-13536(1993).
SQ SEQUENCE 20 AA; 1928 MW; 876B4D50DD80706B CRC64;

Query Match 26.0%; Score 13; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 19 PN 20

RESULT 13
Q9UC66 PRELIMINARY; PRT; 20 AA.
AC Q9UC66;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 33 kDa extracellular matrix-associated serine proteinase inhibitor
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95177668; PubMed=7872799;
RA Rao C.N., Liu Y.Y., Peavey C.L., Woodley D.T.;
RA "Novel extracellular matrix-associated serine proteinase inhibitors
RT from human skin fibroblasts."
RL Arch. Biochem. Biophys. 317:311-314(1995).
SQ SEQUENCE 20 AA; 2157 MW; 893B8E96AB0930F CRC64;

Query Match 26.0%; Score 13; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 6 PN 7

RESULT 14
Q9TG3 PRELIMINARY; PRT; 20 AA.
AC Q9TG3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Galactocerebrosidase (Fragment).
OS CALC.
OC Ateles belzebuth chamek (Chamek spider monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateleinae; Ateles.
OX NCBI_TaxID=118643;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20169179; PubMed=10702662;
RA Canavez F.C., Moreira M.A., Bonvicino C.R., Parham P., Seunarez H.N.;
RT "Evolutionary disruptions of human syntenic groups 3, 12, 14, and 15
RT in Ateles belzebuth chamek (Platyrrhini, Primates).";
RL Cytogenet. Cell Genet. 87:182-188(1999).
DR EMBL; AF099175; AAF21849.1;
DR InterPro; IPR001286; GH_59.
DR Pfam; PF02057; Glyco_hydro_59; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 20 AA; 2317 MW; EA306655966B58F CRC64;

Query Match 26.0%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 9 PN 10

RESULT 15
Q28079 PRELIMINARY; PRT; 20 AA.
AC Q28079;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Epithelial mucin (Fragment).
CN MUC1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=LACTATING MAMMARY GLAND;
RX MEDLINE=96351712; PubMed=8747930;
RA Spicer A.P., Duhig T., Chilton B.S., Gendler S.J.;
RT "Analysis of mammalian MUC1 genes: reveals potential functionally
RT important domains."
RL Mamm. Genome 6:885-888(1995).
DR EMBL; L41553; AAB48100.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 20 AA; 2055 MW; 0E14465183AB743B CRC64;

Query Match 26.0%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 6 PN 7

RESULT 16
P82666 PRELIMINARY; PRT; 20 AA.
AC P82666;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Mitochondrial 28S ribosomal protein S23 (MRP-S23) (Fragments).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.

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OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE
 RC TISSUE=LIVER;
 RX MEDLINE=20490686; PubMed=10938081;
 RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Koc H.,
 RA Sprengli L.L.;
 RT "A proteomics approach to the identification of mammalian
 RT mitochondrial small subunit ribosomal proteins.";
 RL J. Biol. Chem. 275:32585-32591(2000).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC Ribosomal protein; Mitochondrion.
 KW NON TER
 FT NON CONS 1 1
 FT NON TER 10 11
 FT NON TER 20 20
 SQ SEQUENCE 20 AA; 2249 MW; EC7FE3CA50071EE4 CRC64;

Query Match 26.0%; Score 13; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
 DB 17 PN 18

RESULT 17
 Q8SL60 PRELIMINARY; PRT; 20 AA.
 ID Q8SL60;
 AC Q8SL60;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Peba (Fragment).
 GN PSBA.
 OS Aeonium decorum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Saxifragales; Crassulaceae; Aeonium.
 OX NCBI_TaxID=111149;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mort M.E., Soltis D.E., Soltis P.S., Francisco J., Santos A.;
 RT "Evolution and diversification of the Macaronesian clade of
 RT Crassulaceae.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY082197; AAM13941.1; -.
 KW Chloroplast.
 SQ SEQUENCE 20 AA; 2091 MW; 242BED0A664BBD80 CRC64;

Query Match 26.0%; Score 13; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
 DB 1 PN 2

RESULT 18
 P82163 PRELIMINARY; PRT; 20 AA.
 ID P82163;
 AC P82163;
 DT 01-JUN-2000 (TREMBlrel. 14, Created)
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE Chloroplast 30S ribosomal protein S13 (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.

OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC STRAIN=CV. ALVARO; TISSUE=LEAF.
 RX MEDLINE=20435797; PubMed=10874039;
 RA Yamaguchi K., von Koenig K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 RT the small subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 275:28455-28465(2000).
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -1- MASS SPECTROMETRY: MW=14900; METHOD=MALDI.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 15.5 KDA.
 CC -1- SIMILARITY: BELONGS TO THE S13P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro; IPR001892; Ribosomal_S13.
 DR Pfam; PF00416; Ribosomal_S13; 1.
 DR PROSITE; PS00646; RIBOSOMAL_S13; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON TER 20 20
 SQ SEQUENCE 20 AA; 2401 MW; 96AEF51BE1035106 CRC64;

Query Match 26.0%; Score 13; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
 DB 9 PN 10

RESULT 19
 Q9S8X5 PRELIMINARY; PRT; 20 AA.
 ID Q9S8X5;
 AC Q9S8X5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Vegetative storage protein 94 peptide 2, VSP94=LIPOXYGENASE
 DE (Fragment).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eufrosida 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92361246; PubMed=1822994;
 RA Tranbarger T.J., Franceschi V.R., Hildebrand D.F., Grimes H.D.;
 RT "The soybean 94-kilodalton vegetative storage protein is a
 RT lipoxigenase that is localized in paraveinal mesophyll cell
 RT vacuoles.";
 RL Plant Cell 3:973-987(1991).
 FT NON TER 1 1
 FT NON TER 20 20
 SQ SEQUENCE 20 AA; 2330 MW; B889A8684EAD0968 CRC64;

Query Match 26.0%; Score 13; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
 DB 15 PN 16

RESULT 20
 Q9S8R2 PRELIMINARY; PRT; 20 AA.
 ID Q9S8R2;
 AC Q9S8R2;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)

DE Starch branching enzyme (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94009663; PubMed=8405428;
 RA Khoshnoodi J., Ek B., Raak L., Larsson H.;
 RT "Characterization of the 97 and 103 kDa forms of starch branching
 enzyme from potato tubers.";
 RL FEBS Lett. 332:132-138(1993).
 SQ SEQUENCE 20 AA; 2339 MW; 0C69903743FC686D CRC64;

Query Match
 Best Local Similarity 40.0%; Score 13; DB 10; Length 20;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
 Db 14 PSERY 18

RESULT 21
 OQOVG2 PRELIMINARY; PRT; 20 AA.
 AC OQOVG2;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE P100 (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92105130; PubMed=1722209;
 RA Traub L.M., Sagi-Eisenberg R.;
 RT "Purification of p100, a protein antigenically related to the signal
 transducing G proteins Gt and Gi. Evidence for an adaptin-like
 protein.";
 RL J. Biol. Chem. 266:24642-24649(1991).
 FT NON_TER 1
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2141 MW; 9BE4D27AC31BF0B CRC64;

Query Match
 Best Local Similarity 26.0%; Score 13; DB 11; Length 20;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 Db 16 PN 17

RESULT 22
 OQOVF6 PRELIMINARY; PRT; 20 AA.
 AC OQOVF6;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Carbonic anhydrase IV, CA IV (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92147688; PubMed=1737787;
 RA Wahed A., Zhu X.L., Sly W.S.;

RT "Membrane-associated carbonic anhydrase from rat lung. Purification,
 RT characterization, tissue distribution, and comparison with carbonic
 RT anhydrase IIs of other mammals.";
 RL J. Biol. Chem. 267:3308-3311(1992).
 FT NON_TER 1
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2275 MW; 6CB2AC1CD44DEB65 CRC64;

Query Match
 Best Local Similarity 26.0%; Score 13; DB 11; Length 20;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 Db 13 PN 14

RESULT 23
 OQ5096 PRELIMINARY; PRT; 20 AA.
 AC OQ5096;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Punta Toro phlebovirus nonstructural (NS) protein (Fragment).
 OS Punta Toro phlebovirus.
 OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
 OX NCBI_TaxID=11587;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Emery V.C., Bishop D.H.L.;
 RT "Characterization of Punta Toro S mRNA species and identification of
 RT an inverted complementary sequence in the intergenic region of Punta
 RT Toro phlebovirus ambisense S RNA that is involved in mRNA
 RT transcription termination.";
 RL Virology 156:1-11(1987).
 DR EMBL; M16579; AAA47113.1; -.
 FT NON_TER 1
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2243 MW; ADD376276BC72D96 CRC64;

Query Match
 Best Local Similarity 26.0%; Score 13; DB 12; Length 20;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 Db 8 PN 9

RESULT 24
 OQ4860 PRELIMINARY; PRT; 20 AA.
 AC OQ4860;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Hypothetical 2.0 kDa protein (Fragment).
 OS unidentified human poliovirus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 OC Enterovirus.
 OX NCBI_TaxID=40278;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87169734; PubMed=3031313;
 RA Kuge S., Saito I., Nomoto A.;
 RT "Primary structure of poliovirus defective-interfering particle
 RT genomes and possible generation mechanisms of the particles.";
 RL J. Mol. Biol. 192:473-487(1996).
 DR EMBL; M30217; AAA66826.1; -.
 KW Hypothetical protein.
 FT NON_TER 1
 FT NON_TER 20

SQ SEQUENCE 20 AA; 1997 MW; 07546B9F075818F CRC64;

Query Match 26.0%; Score 13; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 10 PN 11

RESULT 25

Q65710 PRELIMINARY; PRT; 20 AA.

AC 065710;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE ORF5 (Fragment).
OS Berne virus (BBV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Torovirus.
OX NCBI_TaxID=11156;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=9080137; PubMed=2293666;
RA Snider E.J., Horzinek M.C., Span W.J.M.;
RT "A 3'-coterminal nested set of independently transcribed mRNAs is
RL J. Virol. 64:331-338(1990).
DR EMBL; M3503; AAA42816.1; -.
FT NON TER 20
SQ SEQUENCE 20 AA; 2141 MW; FAC1CA3A8FF6EBDE CRC64;

Query Match 26.0%; Score 13; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 7 PN 8

RESULT 26

Q9PRN6 PRELIMINARY; PRT; 20 AA.

AC 09PRN6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE Urotensin I homolog.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OX NCBI_TaxID=7830;
RN (1)
RP SEQUENCE.
RX MEDLINE=96051495; PubMed=8536945;
RA Waugh D., Anderson G., Armour K.J., Balment R.J., Hazon N.,
RA Conlon J.M.;
RT "A peptide from the caudal neurosecretory system of the dogfish
RT Scyliorhinus canicula that is structurally related to urotensin I."
RL Gen. Comp. Endocrinol. 99:333-339(1995).
SQ SEQUENCE 20 AA; 2305 MW; 77A92D52817B97B7 CRC64;

Query Match 26.0%; Score 13; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 5 PN 6

RESULT 27

Q9PRU0 PRELIMINARY; PRT; 20 AA.

AC 09PRU0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Osteocalcin (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN (1)
RP SEQUENCE.
RX MEDLINE=95209705; PubMed=7695644;
RA Gotoh Y., Saito E., Glimcher M.J., Gerstenfeld L.C.;
RT "Characterization of the major non-collagenous proteins of chicken
RT bone: identification of a novel 60 kDa non-collagenous
RT phosphoprotein."
RL Biochem. Biophys. Res. Commun. 208:863-870(1995).
SQ SEQUENCE 20 AA; 2078 MW; 2A519C73A76EB9DC CRC64;

Query Match 26.0%; Score 13; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 13 PN 14

RESULT 28

Q9PRR4 PRELIMINARY; PRT; 20 AA.

AC 09PRR4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2002 (TREMBLrel. 20, Last annotation update)
DE Elastase isoform EI (Fragment).
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OX NCBI_TaxID=7830;
RN (1)
RP SEQUENCE.
RX MEDLINE=96124568; PubMed=8541981;
RA Smine A., Le Gal Y.;
RT "Purification and characterization of two pancreatic elastase isoforms
RT from dogfish (Scyliorhinus canicula)."
RL Mol. Mar. Biol. Biotechnol. 4:295-303(1995).
DR HSSP; P00772; IEAI.
DR InterPro; IPR001254; Ser protease_Try.
DR Pfam; PF00089; trypsin; I.
KW Hydrolase; Serine protease.
SQ SEQUENCE 20 AA; 2275 MW; 4DA4A173DA29336 CRC64;

Query Match 26.0%; Score 13; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 9 PN 10

RESULT 29

Q9PRR3 PRELIMINARY; PRT; 20 AA.

ID 09PRR3;
AC 09PRR3;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Elastase isoform EII (Fragment).
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes;
 OC Scyliorhinidae; Scyliorhinus.
 RN NCBI_TaxID=7830;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96124568; PubMed=8541981;
 RA Smithe A., Le Gal Y.;
 RT "Purification and characterization of two pancreatic elastase isoforms
 from dogfish (Scyliorhinus canicula)".
 RT Mol. Mar. Biol. Biotechnol. 4:295-303(1995).
 RL HSP; P00772; IEAI.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00089; trypsin; 1.
 KW Hydrolase; Serine protease.
 SQ SEQUENCE 20 AA; 2260 MW; 4DA4A16586F39336 CRC64;

Query Match 26.0%; Score 13; DB 13; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 ||
 DB 9 PN 10

RESULT 30

O9PRT8 PRELIMINARY; PRT; 20 AA.
 AC O9PRT8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Collagenolytic serine proteinase (Fragment).
 OS Gadus morhua (Atlantic cod).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
 RN NCBI_TaxID=8049;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95268699; PubMed=7749622;
 RA Kristjansson M.M., Gutmundsdottir S., Fox J.W., Bjarnason J.B.;
 RT "Characterization of a collagenolytic serine proteinase from the
 Atlantic cod (Gadus morhua)".
 RT Comp. Biochem. Physiol. 110B:707-717(1995).
 RL NON_TER 1
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2364 MW; 6FFC0365A5269269 CRC64;

Query Match 26.0%; Score 13; DB 13; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 ||
 DB 9 PN 10

RESULT 31

O9DYR0 PRELIMINARY; PRT; 20 AA.
 AC O9DYR0;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Gag polyprotein (Fragment).
 GN Gag.

OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20461476; PubMed=11005867;
 RA Martinez-Picado J., Despasquale M.P., Kartsonis N., Hanna G.J.,
 RA Wong J., Finzi D., Rosenberg E., Gunthard H.F., Sutton L., Savara A.,
 RA Petropoulos C.J., Hellmann N., Walker B.D., Richman D.D.,
 RA Siliciano R., D'Agula R.T.;
 RT "Antiretroviral resistance during successful therapy of HIV type 1
 infection."
 RT Proc. Natl. Acad. Sci. U.S.A. 97:10948-10953(2000).
 RL EMBL; AF292884; AAG25530.1; .
 DR Polyprotein.
 KW Polyprotein.
 FT NON_TER 1
 SQ SEQUENCE 20 AA; 2436 MW; CODEC0F0E88539F CRC64;

Query Match 26.0%; Score 13; DB 15; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 ||
 DB 15 PN 16

RESULT 32

O9X3D3 PRELIMINARY; PRT; 21 AA.
 AC O9X3D3;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE Cytochrome b6/f complex subunit IV (Fragment).
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 RN NCBI_TaxID=1220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Urbach E., Chisholm S.W.;
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically
 sorted from the Sargasso Sea and Gulf Stream."
 RL Limnol. Oceanogr. 43:1615-1630(1998).
 DR EMBL; AF070135; AAD20745.1; .
 FT NON_TER 21
 SQ SEQUENCE 21 AA; 2281 MW; CC946FFCC03C474F CRC64;

Query Match 26.0%; Score 13; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 ||
 DB 7 PN 8

RESULT 33

O9X3E5 PRELIMINARY; PRT; 21 AA.
 AC O9X3E5;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE Cytochrome b6/f complex subunit IV (Fragment).
 GN PETD.
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 RN NCBI_TaxID=1220;
 RN [1]

```

RP  SEQUENCE FROM N.A.
RA  Urbach E., Chisholm S.W.;
RT  "Genetic diversity in Prochlorococcus populations flow cytometrically
RL  sorted from the Sargasso Sea and Gulf Stream.";
DR  Limnol. Oceanog. 43:1615-1630(1998).
EMBL; AF070144; AAD20761.1; -.
FT  NON TER          21
SQ  SEQUENCE          21 AA; 2471 MW; CC834CE2A52C474F CRC64;

Query Match          26.0%; Score 13; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 PN 2
    ||
    7 PN 8

Db

RESULT 34
O9X3G5  PRELIMINARY; PRT; 21 AA.
AC  O9X3G5;
DT  01-NOV-1999 (TREMBlrel. 12, Created)
DT  01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE  Cytochrome b6/f complex subunit IV (Fragment).
GN  PETD.
OS  Prochlorococcus sp.
OC  Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OX  Prochlorococcus.
NCBI_TaxID=1220;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Urbach E., Chisholm S.W.;
RT  "Genetic diversity in Prochlorococcus populations flow cytometrically
RL  sorted from the Sargasso Sea and Gulf Stream.";
DR  Limnol. Oceanog. 43:1615-1630(1998).
EMBL; AF070159; AAD23205.1; -.
FT  NON TER          21
SQ  SEQUENCE          21 AA; 2283 MW; CC97B526F03C474F CRC64;

Query Match          26.0%; Score 13; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 PN 2
    ||
    7 PN 8

Db

RESULT 35
O9X3H2  PRELIMINARY; PRT; 21 AA.
AC  O9X3H2;
DT  01-NOV-1999 (TREMBlrel. 12, Created)
DT  01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE  Cytochrome b6/f complex subunit IV (Fragment).
GN  PETD.
OS  Prochlorococcus sp.
OC  Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OX  Prochlorococcus.
NCBI_TaxID=1220;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Urbach E., Chisholm S.W.;
RT  "Genetic diversity in Prochlorococcus populations flow cytometrically
RL  sorted from the Sargasso Sea and Gulf Stream.";
DR  Limnol. Oceanog. 43:1615-1630(1998).
EMBL; AF070164; AAD23214.1; -.
FT  NON TER          21
SQ  SEQUENCE          21 AA; 2337 MW; DE38B626F03C474F CRC64;

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Query Match          26.0%; Score 13; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 PN 2
    ||
    7 PN 8

Db

RESULT 36
O9X3J7  PRELIMINARY; PRT; 21 AA.
AC  O9X3J7;
DT  01-NOV-1999 (TREMBlrel. 12, Created)
DT  01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE  Cytochrome b6/f complex subunit IV (Fragment).
GN  PETD.
OS  Prochlorococcus sp.
OC  Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OX  Prochlorococcus.
NCBI_TaxID=1220;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Urbach E., Chisholm S.W.;
RT  "Genetic diversity in Prochlorococcus populations flow cytometrically
RL  sorted from the Sargasso Sea and Gulf Stream.";
DR  Limnol. Oceanog. 43:1615-1630(1998).
EMBL; AF070189; AAD23226.1; -.
FT  NON TER          21
SQ  SEQUENCE          21 AA; 2401 MW; CC947A32E52C474F CRC64;

Query Match          26.0%; Score 13; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 PN 2
    ||
    7 PN 8

Db

RESULT 37
O9X3K7  PRELIMINARY; PRT; 21 AA.
AC  O9X3K7;
DT  01-NOV-1999 (TREMBlrel. 12, Created)
DT  01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE  Cytochrome b6/f complex subunit IV (Fragment).
GN  PETD.
OS  Prochlorococcus sp.
OC  Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OX  Prochlorococcus.
NCBI_TaxID=1220;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Urbach E., Chisholm S.W.;
RT  "Genetic diversity in Prochlorococcus populations flow cytometrically
RL  sorted from the Sargasso Sea and Gulf Stream.";
DR  Limnol. Oceanog. 43:1615-1630(1998).
EMBL; AF070199; AAD23243.1; -.
FT  NON TER          21
SQ  SEQUENCE          21 AA; 2279 MW; CC946C4A203C474F CRC64;

Query Match          26.0%; Score 13; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 PN 2
    ||
    7 PN 8

Db

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RESULT 38
Q44611
ID 044611 PRELIMINARY; PRT; 21 AA.
AC 044611;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Shikimate dehydrogenase (Fragment).
GN AROE.
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95212914; PubMed=7535281;
RA Roubaksh D., Baumann P.;
RT "Characterization of a putative 23S-5S rRNA operon of Buchnera
RT aphidicola (endosymbiont of aphids) unlinked to the 16S rRNA-encoding
RT gene."
RL Gene 155:107-112(1995).
DR EMBL; U10500; AAA79129.1; -.
FT NON TER 1
SQ SEQUENCE 21 AA; 2614 MW; 1A1B28CE9D8007A CRC64;

Query Match 26.0%; Score 13; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 10 PN 11

RESULT 39
Q9WM36
ID Q9WM36 PRELIMINARY; PRT; 21 AA.
AC Q9WM36;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE Cytochrome B6/F complex subunit IV (Fragment).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream."
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070207; AAD23256.1; -.
DR EMBL; AF070140; AAD20754.1; -.
DR EMBL; AF070177; AAD20794.1; -.
FT NON TER 21
SQ SEQUENCE 21 AA; 2293 MW; CC947A26F03C474F CRC64;

Query Match 26.0%; Score 13; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 7 PN 8

RESULT 40
Q9R500
ID Q9R500 PRELIMINARY; PRT; 21 AA.
AC Q9R500;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

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DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PROTOPECTINASE-R (EC 4.2.2.10) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
NCBI_TaxID=1423;
RN [1]
RP SEQUENCE.
RX MEDLINE=94169516; PubMed=7764545;
RA Sakamoto T., Hours R.A., Sakai T.;
RL Biosci. Biotechnol. Biochem. 58:353-358(1994).
SQ SEQUENCE 21 AA; 2176 MW; D6D860EED1A54E90 CRC64;

Query Match 26.0%; Score 13; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 5 PN 6

RESULT 41
Q9R4T3
ID Q9R4T3 PRELIMINARY; PRT; 21 AA.
AC Q9R4T3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Pyridine nucleotide transhydrogenase (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
RN [1]
RP SEQUENCE.
RX MEDLINE=95122409; PubMed=7822223;
RA Deshpande R.G., Khan M.B., Bhat D.A., Navalkar R.G.;
RT "Isolation of a 43 kDa protein from Mycobacterium tuberculosis H37Rv
RT and its identification as a pyridine nucleotide transhydrogenase."
RL J. Appl. Bacteriol. 77:639-643(1994).
DR InterPro; IPR004002; AlAdh_PNT.
DR Pfam; PF01262; AlAdh_PNT; 1.
SQ SEQUENCE 21 AA; 2358 MW; B42598639C2A9BA CRC64;

Query Match 26.0%; Score 13; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 6 PN 7

RESULT 42
Q53014
ID Q53014 PRELIMINARY; PRT; 21 AA.
AC Q53014;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Nitrogenase alpha subunit (NifD) truncated (Fragment).
OS Rhizobium etli.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
NCBI_TaxID=29449;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CE-3;
RA Valdeirama B., Davalos A., Girard L., Morett E., Mora U.;
RT "Regulatory proteins and cis-acting elements involved in the
RT transcriptional control of Rhizobium etli reiterated nif genes."

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RL J. Bacteriol. 178:3119-3126(1996).
 DR EMBL: L13618; AAB07744.1; -.
 FT NON_TER 21
 SQ SEQUENCE 21 AA; 2490 MW; 19282319A357D445 CRC64;

Query Match 26.0%; Score 13; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 DB 8 PN 9

RESULT 43

O9UR89 PRELIMINARY; PRT; 21 AA.
 AC O9UR89;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE Chitinase (Fragment).
 OS Coccidioides immitis.
 OC Coccidioides immitis.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Onygenales; mitosporic Onygenales; Coccidioides.
 OX NCBI_TaxID=5501;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=93293339; PubMed=8514419;
 RA Johnson S.M., Zimmermann C.R., Pappagianis D.;
 RT "Amino-terminal sequence analysis of the Coccidioides immitis
 RT chitinase/immunodiffusion-complement fixation protein.";
 RL Infect. Immun. 61:3090-3092(1993)
 SQ SEQUENCE 21 AA; 2246 MW; 7FC9FFEF1CEDCE97 CRC64;

Query Match 26.0%; Score 13; DB 3; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 DB 7 PN 8

RESULT 44

O9HD54 PRELIMINARY; PRT; 21 AA.
 AC O9HD54;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE Uncharacterized gastric protein ZAS1P (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Zhao J.R., Yan X.J., Cui D.X., Han F.C., Hou Y., Su C.Z.;
 RT "Homo sapiens uncharacterized gastric protein ZAS1P mRNA."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF264624; AAG03016.1; -.
 FT NON_TER 1
 SQ SEQUENCE 21 AA; 2523 MW; 0F6AB3FDB7D7F59 CRC64;

Query Match 26.0%; Score 13; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 DB 16 PN 17

RESULT 45

O12812 PRELIMINARY; PRT; 21 AA.
 AC O12812;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Pregnancy-specific beta-1-glycoprotein 11 C-R domain (Fragment).
 GN PSG11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=95104846; PubMed=7806221;
 RA McLenachan P.A., Rutherford K.J., Beggs K.T., Sims S.E.;
 RT "Characterization of the PSG11 gene.";
 RL Genomics 22:356-363(1994).
 DR EMBL: U04325; AAA78265.1; -.
 FT NON_TER 1
 SQ SEQUENCE 21 AA; 2290 MW; 8684E6166B3B38E5 CRC64;

Query Match 26.0%; Score 13; DB 4; Length 21;
 Best Local Similarity 40.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 PNXXY 5
 DB 4 PQVTV 8

RESULT 46

O9UD00 PRELIMINARY; PRT; 21 AA.
 AC O9UD00;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE CDKN2 protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=95400305; PubMed=7670475;
 RA Gris N.A., van der Velden P.A., Sandkuyl L.A., Prins D.E.,
 RA Weaver-Felhaus J., Kamp A., Bergman W., Frants R.R.;
 RT "Homozygotes for CDKN2 (p16) germline mutation in Dutch familial
 RT melanoma kindreds.";
 RL Nat. Genet. 10:351-353(1995).
 DR HSSP: P42771; IDC2.
 SQ SEQUENCE 21 AA; 2192 MW; 9424A5E1D7DEAF55 CRC64;

Query Match 26.0%; Score 13; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 DB 9 PN 10

RESULT 47

O61553 PRELIMINARY; PRT; 21 AA.
 AC O61553;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Acetylcholinesterase (Fragment).
 GN ACE OR ACHE.
 OS Drosophila mulleri (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OK NCBI_TaxID=7231;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX Baker R.H., Desalle R.,
 RA Baker R.H., Desalle R.,
 RL Syst. Biol. 46:654-673(1997).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX Baker R.H., Desalle R.,
 RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYL-ESTERASE/LIPASE FAMILY.
 DR EMBL: AF050697; AAC05410.1; -.
 DR HSSP: P22303; 2CLD.
 DR Flybase: FBgn024425; Dmnl\Ace.
 DR InterPro: IPR002018; Carboxylesterase.
 DR PROSITE: PS00941; CARBOXYL-ESTERASE_B_2; 1.
 KW Hydrolase.
 FT NON-TER 1 1
 FT NON-TER 21 21
 SQ SEQUENCE 21 AA; 2478 MW; BE017087A5084D0F CRC64;

Query Match 26.0%; Score 13; DB 5; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 DB 5 PN 6
 RESULT 48
 Q9TQZ0 PRELIMINARY; PRT; 21 AA.
 AC Q9TQZ0;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE 90 kDa glycoprotein/GP I11A homolog (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OK NCBI_TaxID=9823;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=96219641; PubMed=8639832;
 RA Thibaudau K., Borche L., Soullion J.P., Blanchard D.;
 RT "Characterization of porcine platelet glycoproteins recognized by
 human natural 'anti-gal' antibodies."
 RL Blood 87:4636-4642(1996).
 SQ SEQUENCE 21 AA; 2168 MW; AFB4AC17A262D2A2 CRC64;

Query Match 26.0%; Score 13; DB 6; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 DB 2 PN 3
 RESULT 49
 Q9TRP5 PRELIMINARY; PRT; 21 AA.
 AC Q9TRP5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE 2-oxoglutarate dehydrogenase, E1 (Fragment).

OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OK NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=92371429; PubMed=1505515;
 RA Rice J.E., Dunbar B., Lindsay J.G.;
 RT "Sequences directing dihydrolipamide dehydrogenase (E3) binding are
 located on the 2-oxoglutarate dehydrogenase (E1) component of the
 RT mammalian 2-oxoglutarate dehydrogenase multienzyme complex."
 RL EMBO J. 11:3229-3235(1992).
 SQ SEQUENCE 21 AA; 2165 MW; 3782319620C406C2 CRC64;

Query Match 26.0%; Score 13; DB 6; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 DB 8 PN 9

RESULT 50
 Q8WLR1 PRELIMINARY; PRT; 21 AA.
 AC Q8WLR1;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Major histocompatibility complex class I (Fragment).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX TISSUE=BLOOD;
 RX MEDLINE=97246738; PubMed=9089103;
 RA Vargas-Alarcon G., Gomez-Casado E., Martinez-Laso J., Granados J.,
 RA Layrisse Z., Alegre R., Arnal-Villena A.;
 RT "Differences in intron 2 sequences between B*39061 and B*39062 in
 RT Amerindians: comparison with those of B*3901, B*5101, and B*52012
 RT alleles."
 RL Immunogenetics 45:436-439(1997).
 DR EMBL: L77205; AAL40076.1; -.
 FT NON-TER 1 1
 FT NON-TER 21 21
 SQ SEQUENCE 21 AA; 1972 MW; 5941EC53ECF3A73D CRC64;

Query Match 26.0%; Score 13; DB 7; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
 DB 3 PN 4

Search completed: June 11, 2003, 07:43:18
 Job time : 33 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 11, 2003, 07:42:19 ; Search time 34 Seconds

(without alignments)
82.302 Million cell updates/sec

Title: US-09-883-727a-127

Perfect score: 50
Sequence: 1 PNMXXXXXXXXXXXXXXXXX 21

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 19888

Minimum DB seq length: 20

Maximum DB seq length: 21

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

A_Geneseq_101002:*

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2: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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4: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
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21: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	46.0	20	23	AAE20076
2	23	46.0	21	23	AAE20074
3	19	38.0	20	15	AAAR45568
4	19	38.0	20	15	AAAR45569
5	19	38.0	20	16	AAAR82518
6	19	38.0	20	16	AAAR82517
7	19	38.0	21	23	ABG35294
8	19	38.0	21	23	AAU89742
9	18	36.0	20	23	AAW89167
10	18	36.0	20	23	AAW47454

11	18	36.0	21	15	AAE0572	Human SP1(A) with
12	18	36.0	21	16	AAE79990	ARH1 peptide mimet
13	18	36.0	21	23	ABG35291	Human PAR1 type th
14	18	36.0	21	23	ABG35293	Human PAR1 type th
15	18	36.0	21	23	ABG35295	Human PAR1 type th
16	18	36.0	21	23	ABG35296	Human PAR1 type th
17	18	36.0	21	23	AAU76681	Influenza A virus
18	17	34.0	20	23	ABP46808	Human Blys binding
19	17	34.0	20	23	ABP46832	Human Blys binding
20	17	34.0	21	16	AAE79996	Human Blys binding
21	17	34.0	21	23	ABG66207	Ige Fcεpsillon Ri b
22	17	34.0	21	23	ABG66289	Ige Fcεpsillon Ri b
23	17	34.0	21	23	ABG66416	Ige Fcεpsillon Ri b
24	16	32.0	20	20	AAW78202	Human secreted pro
25	16	32.0	20	22	AAU02715	Human secreted pro
26	16	32.0	21	23	ABP46758	CDR region of anti
27	16	32.0	21	23	AAE20075	Human Blys binding
28	16	32.0	21	23	AAE20125	Complement C1s inh
29	15	30.0	20	14	AAE33444	Complement C1s inh
30	15	30.0	20	16	AAE84491	HCV NS5 fragment e
31	15	30.0	20	17	AAE91009	Hepatitis C virus
32	15	30.0	20	21	AAE67694	HCV E2 peptide E2-
33	15	30.0	20	21	AAE67767	Peptide #94 for de
34	15	30.0	20	22	AAE66943	Peptide #167 for d
35	15	30.0	20	22	AAE55825	RSV M2 ORF2 fragme
36	15	30.0	20	22	AAE57687	PL peptide #36. S
37	15	30.0	20	22	AAE58097	CC CKR-4 PL peptid
38	15	30.0	21	10	AAE93300	Sequence of Chalm
39	15	30.0	21	10	AAE93322	Sequence of Chalm
40	15	30.0	21	10	AAE98419	Chlamydia trachoma
41	15	30.0	21	10	AAE98427	Sequence of C. tra
42	15	30.0	21	19	AAW46505	Sequence of C. tra
43	15	30.0	21	20	AAV05690	Peptide 5 of the a
44	15	30.0	21	20	AAW73879	Human tumor necro
45	15	30.0	21	21	AAE23881	C. trichomatis ser
46	15	30.0	21	21	AAE23892	C. trichomatis ser
47	15	30.0	21	21	AAE23903	Artificial sequec
48	15	30.0	21	23	ABG68768	Artificial sequec
49	15	30.0	21	23	ABG68776	C. trichomatis ser
50	15	30.0	21	23	ABG68826	C. trichomatis ser
51	14	28.0	20	13	AAE26165	Chlamydia trachoma
52	14	28.0	20	14	AAE33097	Tuberculosis antib
53	14	28.0	20	14	AAE33098	Human cytomegalovi
54	14	28.0	20	15	AAE49325	Human cytomegalovi
55	14	28.0	20	15	AAE49325	MSE position 111-
56	14	28.0	20	15	AAE49343	DR1 beta chain pos
57	14	28.0	20	15	AAE56620	Alginic acid Al-I
58	14	28.0	20	15	AAE61237	Alginic acid Al-I
59	14	28.0	20	16	AAE61237	N-terminal fragmen
60	14	28.0	20	17	AAE61237	SRC SH3 domain bin
61	14	28.0	20	17	AAE61237	BRCA1 antigen C-20
62	14	28.0	20	18	AAE61237	Fragment of human
63	14	28.0	20	20	AAE61237	HHV8 ORF K8.1-deri
64	14	28.0	20	21	AAE61237	Human MHC class II
65	14	28.0	20	22	AAE61237	Human immune/haema
66	14	28.0	20	22	AAE61237	Internal peptide o
67	14	28.0	20	22	AAE61237	Trypsin inhibitor
68	14	28.0	20	23	ABG62847	Ligand/receptor sp
69	14	28.0	20	23	ABG62848	Ligand/receptor sp
70	14	28.0	20	23	ABP47042	Human Blys binding
71	14	28.0	21	14	AAE33099	Human cytomegalovi
72	14	28.0	21	16	AAE80001	ARH1 peptide mimet
73	14	28.0	21	17	AAE05296	Human Blys binding
74	14	28.0	21	19	AAE20896	Human Blys binding
75	14	28.0	21	19	AAE20896	Human Blys binding
76	14	28.0	21	20	AAE54712	Human Blys binding
77	14	28.0	21	20	AAE54712	Human Blys binding
78	14	28.0	21	21	AAE44711	Human Blys binding
79	14	28.0	21	21	AAE44711	Human Blys binding
80	14	28.0	21	21	AAE44711	Human Blys binding
81	14	28.0	21	21	AAE44711	Human Blys binding
82	14	28.0	21	22	ABE41150	Staphylococcus aur
83	14	28.0	21	22	ABE41150	Protein #7186 enco
84	14	28.0	21	22	ABE41150	Human DNA ligase I
85	14	28.0	21	22	ABE41150	Human MUC1 immunog

84	14	28.0	21	22	AAM62006	Human brain expres
85	14	28.0	21	22	AAM74810	Human bone marrow
86	14	28.0	21	22	AAK34926	Peptide #8963 enco
87	14	28.0	21	22	AAAB81503	Stachybotrys chart
88	14	28.0	21	22	AAAB20098	Stachybotrys chart
89	14	28.0	21	22	ABG659513	Staphylococcus aur
90	14	28.0	21	23	ABG65640	Phage displayed g3
91	14	28.0	21	23	ABG65641	Phage displayed g3
92	14	28.0	21	23	ABG44600	Human peptide enco
93	14	28.0	21	23	ABP46752	Human Blys binding
94	14	28.0	21	23	ABP46999	Human Blys binding
95	14	28.0	21	23	ABB75755	Phenol oxidising e
96	14	28.0	21	23	AAU88130	Stachybotrys chart
97	14	28.0	21	23	AAU89042	Insulin/insulin-11
98	14	28.0	21	23	AAU89791	Insulin/insulin-11
99	14	28.0	21	23	AAU89838	Insulin/insulin-11
100	14	28.0	21	23	AAU89838	Insulin/insulin-11
101	14	28.0	21	23	AAU75035	RALV Env protein v
102	13	26.0	20	4	AAAP30108	Sequence of VPI ca
103	13	26.0	20	5	AAAP40161	Sequence at antigen
104	13	26.0	20	8	AAAP70104	Staphylococcus aur
105	13	26.0	20	9	AAAP82905	Acetylcholinestera
106	13	26.0	20	9	AAAP81801	Sequence of peptid
107	13	26.0	20	9	AAAP81802	Sequence of peptid
108	13	26.0	20	9	AAAP81803	Sequence of peptid
109	13	26.0	20	9	AAAP80173	Sequence of p86 po
110	13	26.0	20	9	AAAP80174	Sequence of p87 po
111	13	26.0	20	10	AAAP93077	Sequence surroundi
112	13	26.0	20	10	AAAP90686	Hirudin fragment
113	13	26.0	20	10	AAAP97786	Sequence encoded b
114	13	26.0	20	11	AAAR04963	Papilloma virus ty
115	13	26.0	20	11	AAAR04964	Papilloma virus ty
116	13	26.0	20	11	AAAR05006	Papilloma virus ty
117	13	26.0	20	11	AAAR06985	Papilloma virus ty
118	13	26.0	20	12	AAAR11384	Recombinant 276-29
119	13	26.0	20	12	AAAR15347	Immunopeptide #8 d
120	13	26.0	20	12	AAAR15566	Immunopeptide #1 d
121	13	26.0	20	13	AAAR11073	FMVY peptide-0. S
122	13	26.0	20	13	AAAR13342	Glucosyl transfera
123	13	26.0	20	13	AAAR33888	N-terminal sequenc
124	13	26.0	20	13	AAAR26534	Sequence of peptid
125	13	26.0	20	13	AAAR52829	CNBR peptide #1 of
126	13	26.0	20	13	AAAR28159	Sugar beet beta-1,
127	13	26.0	20	14	AAAY21537	Control peptide de
128	13	26.0	20	14	AAAR48935	Nerve growth facto
129	13	26.0	20	14	AAAR4103	Complement C3 comp
130	13	26.0	20	14	AAAR4103	INHIB N-terminal.
131	13	26.0	20	14	AAAR33726	Peptide EVC38. Sy
132	13	26.0	20	14	AAAR33406	T helper peptide H
133	13	26.0	20	14	AAAR33303	Cytotoxic T-lympho
134	13	26.0	20	14	AAAR37982	P. vivax circumspo
135	13	26.0	20	14	AAAR37983	P. vivax circumspo
136	13	26.0	20	14	AAAR38293	MAHB hepatitis vir
137	13	26.0	20	14	AAAR39886	HLV-I and HTLV-II
138	13	26.0	20	14	AAAR41090	Snake venom thromb
139	13	26.0	20	14	AAAR52019	Aniher glucosyltr
140	13	26.0	20	15	AAAR44171	Micrococcal putres
141	13	26.0	20	15	AAAR53378	Neurotrophic facto
142	13	26.0	20	15	AAAR53774	GS150-169 ('S2")
143	13	26.0	20	15	AAAR45191	EHV-1 derived pepti
144	13	26.0	20	15	AAAR46062	Cry j I pollen all
145	13	26.0	20	15	AAAR45563	Cry j I pollen all
146	13	26.0	20	15	AAAR45564	Cry j I

ALIGNMENTS

ID	AAE20076	standard; peptide; 20 AA.
XX	AAE20076;	
AC	18-JUN-2002 (first entry)	
DT	Complement C1s inhibitor peptide #4.	
XX		
DE	Complement C1s; therapeutic; adult respiratory distress syndrome; stroke;	
KW	preservative; ischaemia-reperfusion injury; myocardial infarct; sepsis;	
KW	hyperacute rejection; rheumatoid arthritis; burn; wound healing; asthma;	
KW	systemic lupus erythematosus; SLE; haemolytic anaemia; serum sickness;	
KW	restenosis; myasthenia gravis.	
OS	Unidentified.	
XX		
PH	Key	Location/Qualifiers
FT	Modified-site	3 /label= Asp, Glu
FT	Modified-site	4 /label= Asp, Glu
FT	Modified-site	6 /note= "Sulphated Phe"
FT	Modified-site	7 /note= "Sulphated Tyr"
FT	Modified-site	8 /note= "2-sulphotyrosine"
FT	Modified-site	9 /label= Asp, Glu
FT	Modified-site	10 /label= Asp, Glu
FT	Modified-site	12 /note= "Sulphated Phe"
FT	Modified-site	13 /note= "Sulphated Tyr"
FT	Modified-site	14 /note= "2-sulphotyrosine"
FT	Modified-site	15 /label= Asp, Glu
FT	Modified-site	17 /note= "Sulphated Phe"
FT	Modified-site	18 /note= "Sulphated Tyr"
FT	Modified-site	19 /note= "2-sulphotyrosine"
FT	Modified-site	20 /label= Asp, Glu
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PN	WO200198365-A2.	
XX		
PD	27-DEC-2001.	
XX		
PP	18-JUN-2001; 2001WO-US19405.	
XX		
PR	21-JUN-2000; 2000US-212998P.	
XX		
PA	(ZYMO) ZYMOGENETICS INC.	
XX		
PI	West RR, Shepard PO, Fox BA;	
XX		
DR	WPI; 2002-241177/29.	
XX		

New complement C1s inhibitor polypeptides for treating diseases in which complement activation has been shown to occur, e.g. adult respiratory distress syndrome, ischaemia-reperfusion injury, asthma, or

RESULT 1

CC Molecules that inhibit complement may be used for treating diseases
CC in which complement activation has been shown to occur, e.g., adult
CC respiratory distress syndrome, ischemia-reperfusion injury (myocardial
CC infarct, stroke), hyperacute rejection, sepsis, burns, wound healing,
CC asthma, restenosis, rheumatoid arthritis, systemic lupus erythematosus,
CC serum sickness, haemolytic anaemias, or myasthenia gravis. The present
CC sequence is complement C1s inhibitor peptide.

SQ Sequence 20 AA:

Query Match 46.0%: Score 23; DB 23; Length 20;

Best Local Similarity 62.5%: Pred. No. 39;

Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 PNXXYXXXXXXYY 16
1 PNXYYFYXXYY 16

RESULT 2

ID AAE20074 standard; peptide; 21 AA.

AC AAE20074;

DT 18-JUN-2002 (first entry)

DE Complement C1s inhibitor peptide #2.

KM Complement C1s; therapeutic; adult respiratory distress syndrome; stroke;
KM preservative; ischemia-reperfusion injury; myocardial infarct; sepsis;
KM hyperacute rejection; rheumatoid arthritis; burn; wound healing; asthma;
KM systemic lupus erythematosus; SLE; haemolytic anaemia; serum sickness;
KM restenosis; myasthenia gravis.

XX Unidentified.

FH Key Location/Qualifiers

FT Modified-site 3 /label= Asp, Glu

FT Modified-site 4 /label= Asp, Glu

FT Modified-site 6 /note= "Sulphated Phe"

FT Modified-site 7 /note= "Sulphated Tyr"

FT Modified-site 8 /note= "2-sulphotyrosine"

FT Modified-site 9 /label= Asp, Glu

FT Modified-site 10 /label= Asp, Glu

FT Modified-site 12 /note= "Sulphated Phe"

FT Modified-site 13 /note= "Sulphated Tyr"

FT Modified-site 14 /note= "2-sulphotyrosine"

FT Modified-site 15 /label= Asp, Glu

FT Modified-site 17 /note= "Sulphated Phe"

FT Modified-site 18 /note= "Sulphated Tyr"

FT Modified-site 19 /note= "2-sulphotyrosine"

FT Modified-site 20 /label= Asp, Glu

FT Misc-difference 21 /label= Asp, Glu

FT /note= "Optionally absent"

PN WO200198365-A2.

XX 27-DEC-2001.
PD .
XX 18-JUN-2001; 2001WO-US19405.

PR 21-JUN-2000; 2000US-212998P.

XX (ZYMO) ZYMOGENETICS INC.

PA West RR, Sheppard PO, Fox BA;

XX WPI; 2002-241177/29.

DR WPI; 2002-241177/29.

PT New complement C1s inhibitor polypeptides for treating diseases in

PT which complement activation has been shown to occur, e.g., adult

PT respiratory distress syndrome, ischemia-reperfusion injury, asthma, or

PT sepsis

PS Claim 1; Page 49; 99pp; English.

CC The invention relates to a polypeptide that inhibits complement C1s. The
CC inhibitory peptides are useful as therapeutic agents, as preservatives
CC in blood samples, and in affinity purification procedures to isolate C1s.
CC Molecules that inhibit complement may be used for treating diseases
CC in which complement activation has been shown to occur, e.g., adult
CC respiratory distress syndrome, ischemia-reperfusion injury (myocardial
CC infarct, stroke), hyperacute rejection, sepsis, burns, wound healing,
CC asthma, restenosis, rheumatoid arthritis, systemic lupus erythematosus,
CC serum sickness, haemolytic anaemias, or myasthenia gravis. The present
CC sequence is complement C1s inhibitor peptide.

SQ Sequence 21 AA:

Query Match 46.0%: Score 23; DB 23; Length 21;

Best Local Similarity 62.5%: Pred. No. 41;

Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 PNXXYXXXXXXYY 16
1 PNXYYFYXXYY 16

RESULT 3

ID AAR45568 standard; Protein; 20 AA.

AC AAR45568;

DT 13-JUL-1994 (first entry)

DE Cry j I pollen allergen peptide CJI-27.

XX Japanese cedar; detection; allergy; treatment; diagnosis;

XX T cell epitope; sensitivity.

OS Crytomera japonica.

PN WO9401560-A.

XX 20-JAN-1994.

PD 15-JAN-1993; 93WO-US00139.

PF 01-SEP-1992; 92US-0938990.

PR 10-JUL-1992; 92WO-US05661.

XX (IMMU-) IMMUNOLOGIC PHARM CORP.

XX Bond JF, Garman RD, Griffith IJ, Kuo M, Pollock J;

XX WPI; 1994-035066/04..

XX Antigen derived from Japanese cedar pollen allergen Cry j I -

PT contain at least two T cell epitope(s), used to treat or diagnose
PT allergy

PS Claim 1; Fig 13; 137bp; English.

CC The sequence is that of an isolated peptide of the Japanese cedar
CC pollen allergen Cry j I (amino acids 261-280). The peptide, CJI-27,
CC can be used for the treatment and diagnosis of allergies associated
CC with Japanese cedar pollen. It has enhanced therapeutic properties
CC but reduced side effects compared to naturally occurring allergens.

XX Sequence 20 AA;

Query Match

Best Local Similarity 38.0%; Score 19; DB 15; Length 20;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5

DB 11 PNE5Y 15

RESULT 4

AA845569 ID AAR45569 standard; Protein; 20 AA.

AC AAR45569;

DT 13-JUL-1994 (first entry)

DE Cry j I pollen allergen peptide CJI-28.

XX Japanese cedar; detection; allergy; treatment; diagnosis;

OS T cell epitope; sensitivity.

XX Cryptomeria japonica.

PN MO9401560-A.

PD 20-JAN-1994.

PF 15-JAN-1993; 93WO-US00139.

PR 01-SEP-1992; 92US-0938990.

PA 10-JUL-1992; 92WO-US05661.

PI (IMMU-) IMMUNOLOGIC PHARM CORP.

DR Bond JF, Garman RD, Griffith IU, Kuo M, Pollock J;

PT WPI; 1994-035066/04.

PS Antigens derived from Japanese cedar pollen allergen Cry j I -

XX contain at least two T cell epitope(s), used to treat or diagnose

XX allergy

PS Claim 64; Fig 13; 137bp; English.

CC The sequence is that of an isolated peptide of the Japanese cedar

CC pollen allergen Cry j I (amino acids 271-290). The peptide, CJI-28,

CC can be used for the treatment and diagnosis of allergies associated

CC with Japanese cedar pollen. It has enhanced therapeutic properties

CC but reduced side effects compared to naturally occurring allergens.

XX Sequence 20 AA;

Query Match

Best Local Similarity 38.0%; Score 19; DB 15; Length 20;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5

DB 11 PNE5Y 5

RESULT 5

AA82518 ID AAR82518 standard; Protein; 20 AA.

AC AAR82518;

DT 15-APR-1996 (first entry)

DE Cry j I Japanese Cedar pollen allergen peptide fragment (CJI-28).

XX Cry j I; Japanese cedar pollen allergen; modified; drug production;

XX allergy; Cryptomeria japonica.

PN MO9527786-A1.

PD 19-OCT-1995.

PF 06-APR-1995; 95WO-US04249.

PR 06-DEC-1994; 94US-0350225.

PA 08-APR-1994; 94US-0226248.

PI (IMMU-) IMMUNOLOGIC PHARM CORP.

DR Chen X, Evans S, Franzen HM, Kuo M, Powers SP;

PT Shaked Z;

PS WPI; 1995-366391/47.

DE Modified Cryptomeria japonica (Cry j) I peptide(s) - useful for

XX treating allergy to Japanese cedar pollen allergen or

XX immunologically cross reactive allergens

XX Disclosure; Figure 2; 60pp; English.

CC Novel peptides of cry j I have been modified as a part of a

CC preformulation scheme to develop an optimised drug product for

CC therapeutic treatment of humans suffering from allergy to Japanese

CC cedar pollen allergen or an allergen which is immunologically cross

CC reactive with Japanese cedar pollen allergen. Such modified peptides

CC possess certain characteristics which render them particularly

CC suitable for drug product formulation. Peptide fragments of Cry j I,

CC modified and unmodified, are given in AAR82491-R82525. This peptide

CC fragment corresponds to amino acids 271-290 of the allergen mature

XX protein.

XX Sequence 20 AA;

Query Match

Best Local Similarity 38.0%; Score 19; DB 16; Length 20;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5

DB 1 PNE5Y 5

RESULT 6

AA82517 ID AAR82517 standard; Protein; 20 AA.

AC AAR82517;

DT 15-APR-1996 (first entry)

DE Cry j I Japanese Cedar pollen allergen peptide fragment (CJI-27).

XX Cry j I; Japanese cedar pollen allergen; modified; drug production;

XX allergy; Cryptomeria japonica.

CC The invention relates to a method of modulating insulin activity in
CC mammalian cells by administering a peptide that binds the insulin
CC receptor (IR). A composition containing a peptide, optionally expressed
CC from gene therapy vectors, that binds to Site 1 of IR and an insulin
CC agonist are useful for treating diabetes. Also, peptides that are
CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC useful for treating insulin-like growth factor (IGF)-sensitive tumours
CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC receptor agonists are useful for treating neurological diseases.
CC including stroke and diabetic neuropathy. The peptides are also useful in
CC screening for compounds that bind to IR or IGF-1 receptor, potential
CC therapeutics and research reagents. AA08034-AA09057 represent IR
CC and/or IGF-1 receptor-binding peptides and related amino acid sequences
CC of the invention.
CC
SQ Sequence 21 AA:
Query Match 38.0%; Score 19; DB 23; Length 21;
Best Local Similarity 60.0%; Pred. No. 4.2e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 PNXXY 5
| | |
Db 4 PMSFY 8

RESULT 9
AA089167
ID AA089167 standard; peptide: 20 AA.
XX
AC AA089167;
XX
DT 25-MAR-1999 (first entry)
XX
DE Anti-p53 monoclonal antibody 246 CDR2 heavy chain based peptide #1.
XX
KM Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;
XX immune response; tumour associated antigen; metastatic cancer.
XX
OS Mus sp.
XX Synthetic.
XX
PN W09856416-A1.
XX
PD 17-DEC-1998.
XX
PF 09-JUN-1998; 98WO-IL00266.
XX
PR 09-JUN-1997; 97IL-0121041.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Cohen IR, Erez-Alon N, Herkel J, Rotter V, Ruiz RJ;
XX Wolkowicz R;
XX
DR WPI; 1999-070296/06.
XX
PT Use of a monoclonal antibody to a tumour-associated antigen - to
XX induce anti-tumour immunity or elicit an increased immune response
XX to the antigen
XX
PS Claim 9; Page 30; 47pp; English.
XX
CC The present invention describes the use of an immunogen (A) to induce
CC anti-tumour immunity; to elicit an increased immune response to tumour
CC associated antigen (TAA) and/or to induce an immune response to mutant
CC or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody
CC (MAB) to TAA, or its fragment; (ii) a peptide based on a CDR
CC (complementarily determining region) on the heavy or light chain of MAB
CC (able to elicit antibodies to TAA); or (iii) a DNA that encodes the
CC variable (V) region of MAB, in a gene delivery vehicle. The present
CC sequence represents a peptide based on CDR2 of the heavy chain of
CC anti-p53 MAB 246. Also described is a method for generating sequence-

CC specific, anti-DNA antibodies (Ab) by immunising a mammal with a MAB
CC directed to a domain containing a DNA-binding site of a DNA-binding
CC protein. (A) is used to treat a wide variety of primary and metastatic
CC cancers, particularly those where p53 is involved. Ab are used for
CC diagnosis (e.g. to determine critical sequences in animal or plant
CC breeding); to identify bacteria and other parasites; to determine
CC parentage; in gene sequencing and cloning; also possibly for activation
CC of selected therapeutic genes in plants, animals and humans. (A) induce
CC an effective anti-tumour response without causing harm to the patient.
CC The method uses (A) to generate anti-TAA by exploiting the anti-idiotypic
CC network.
CC
SQ Sequence 20 AA:
Query Match 36.0%; Score 18; DB 20; Length 20;
Best Local Similarity 60.0%; Pred. No. 7.2e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 PNXXY 5
| | |
Db 5 PNNGY 9

RESULT 10
AA047454
ID AA047454 standard; peptide: 20 AA.
XX
AC AA047454;
XX
DT 08-FEB-2002 (first entry)
XX
DE Rat kidney repair factor, KRGF1 peptide fragment, TRDH-091-2.
XX
KM Rat; kidney repair factor; KRGF1; antiinflammatory; nephrotoxic;
XX gene therapy; vaccine; kidney damage; kidney failure; inflammation;
XX TRDH-091-2.
XX
OS Rattus norvegicus.
XX
FH Key Location/Qualifiers
FT Modified-site 20
FT /note="C-terminal amide"
XX
PN W0200168817-A1.
XX
PD 20-SEP-2001.
XX
PF 16-MAR-2001; 2001WO-JP02087.
XX
PR 16-MAR-2000; 2000JP-0073632.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Takeuchi K, Kato Y, Sekine S, Kikuchi Y, Sakurada K;
XX WPI; 2002-055101/07.
XX
PT Kidney repair factor KRGF1 for the treatment and diagnosis of damage to
XX kidney tissue comprises monitoring the increased expression in damaged
XX kidney tissue of KRGF1 and antibodies recognizing it -
XX
PS Example 7; Page 115-116; 121pp; Japanese.
XX
CC The present sequence is a peptide fragment of rat kidney repair factor,
CC KRGF1 (AA047452). KRGF1 was found to have increased expression in damaged
CC kidney tissue. KRGF1 can be used for the diagnosis of kidney tissue
CC damage and kidney failure; and for the treatment of damaged/inflamed
CC kidney tissues.
XX
SQ Sequence 20 AA:
Query Match 36.0%; Score 18; DB 23; Length 20;

Best Local Similarity 60.0%; Pred. No. 7.2e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
111
Db 9 PNRFY 13

RESULT 11

AAR60572
ID AAR60572 standard; Protein; 21 AA.

AC AAR60572;

DT 01-APR-1995 (first entry)

DE Human SP1(A) with homology to DRA transcription activation domain.

KM DRA; down-regulated in adenoma; tumor suppressor; colon adenoma;
KM colon adenocarcinoma; diagnostic; therapeutic.

OS Homo sapiens.

PN WO9420616-A.

PD 15-SEP-1994.

PF 04-MAR-1994; 94MO-US01860.

PR 05-MAR-1993; 93US-0026045.

PA (SCHW/) SCHWEINFEST C W.
(USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Papas TS, Schweinfest CW;

DR WPI; 1994-303023/37.

PT Isolated polypeptide that is down regulated in colon
PT adenocarcinomas and adenomas - is used as an indicator of tissue
PT abnormality.

PS Fig 3; Page 28; 41pp; English.

CC The human SP1(A) sequence is homologous to amino acids 620-640
(representing the transcription activation domain) region of
CC the DRA tumor suppressor (AAR60568). DRA can be used as an
CC antigen for the production of monoclonal antibodies, which
CC may then be used diagnostically for detecting the presence/absence
CC of DRA polypeptide in tissue sample. Absence of DRA protein
CC indicates tissue abnormality.

SO Sequence 21 AA;

Query Match 36.0%; Score 18; DB 15; Length 21;
Best Local Similarity 60.0%; Pred. No. 7.5e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
111
Db 14 PNIFY 18

RESULT 12

AAR79990
ID AAR79990 standard; peptide; 21 AA.

AC AAR79990;

DT 01-MAY-1996 (first entry)

DE ARH1 peptide mimotope, mouse T cell receptor, TCR-zeta/*a.

KM Signal transduction; src-family thymidine kinase; lipid kinase;
KM tyrosine kinase; adaptor; inhibition; regulation; immunodeficiency;
KM allergy; inflammation; cancer; autoimmune disease; Epstein-Barr virus;
KM immunoproliferative disease; bovine leukemia virus; EBV; BLV;
KM chronic fatigue syndrome; infectious mononucleosis.

OS Mus sp.

PN WO9524915-A1.

PD 21-SEP-1995.

PF 17-MAR-1995; 95MO-US03438.

PR 17-MAR-1994; 94US-0215116.

PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.

PI Cambier JC, Clark MR, Pleiman CW;

DR WPI; 1995-336809/43.

PT Regulation of signal transduction pathways, esp. involving
PT src-family thymidine kinase - useful for treatment of allergic and
PT inflammatory responses

PS Disclosure; Page 23; 131pp; English.

CC AAR79986-R80004 signal transduction regulatory ARH1 peptide mimetopes.
CC ARH1 peptides and mimetopes of ARH1 peptides are capable of regulating
CC the activity of tyrosine kinases, lipid kinases, thymidine kinases and
CC adaptor molecules. They can be used in a method to regulate signal
CC transduction in such cells as B cells, T cells, macrophages, dendritic
CC cells and pluripotent stem cells. The method allows regulation and
CC treatment of allergic and inflammatory responses, autoimmune disease,
CC immunodeficiency and immunoproliferative diseases, cancer and disease
CC caused by Epstein-Barr and bovine leukemia viruses.

SO Sequence 21 AA;

Query Match 36.0%; Score 18; DB 16; Length 21;
Best Local Similarity 60.0%; Pred. No. 7.5e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
111
Db 9 PNQLY 13

RESULT 13

ABG35291
ID ABG35291 standard; peptide; 21 AA.

AC ABG35291;

DT 15-JUL-2002 (first entry)

DE Human PAR1 type thrombin receptor based peptide #95.

KM PAR1; thrombin receptor; antiinflammatory; cytostatic; human;
KM inflammatory disease; cell proliferative disease.

OS Homo sapiens.

OS Synthetic.

PN JP2002010784-A.

PD 15-JAN-2002.

PF 29-JUN-2000; 2000JP-0196514.

PR 29-JUN-2000; 2000JP-0196514.

PA (TEIJ) TEIJIN LTD.
XX
XX WPI: 2002-321520/36.
XX
PT An inhibitor of cell growth mediated by thrombin used to treat
PT inflammatory and cell proliferative diseases -
XX
PS Example 10; Page 20; 44pp; Japanese.
XX
CC The invention relates to a polypeptide or a compound which can inhibit
CC cell growth caused by thrombin. The polypeptide/compound combines to a
CC specific region of the structure of PAR1 type human thrombin receptor
CC participating to cell growth. Preferably, the compound contains the
CC 52nd to the 56th amino acid sequences at the amino end side of PAR1 type
CC human thrombin receptor ((X4)-Tyr-Glu-Pro-Phe-Trp-(X5) X4, X5 = optional
CC amino acid or peptide sequence). Also included are a modified PAR1 type
CC thrombin receptor gene or its fragment used for obtaining the above
CC polypeptide, a human PAR1 type thrombin receptor protein and its
CC encoding DNA comprising a fully. The polypeptide or the compound is used
CC to treat inflammatory diseases and cell proliferative diseases. The
CC present sequence is a peptide compound of the invention based on the PAR1
CC type thrombin receptor (or a modified version).
XX
SQ Sequence 21 AA;
XX
Query Match 36.0%; Score 18; DB 23; Length 21;
Best Local Similarity 60.0%; Pred. No. 7.5e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 PNXXY 5
DB 2 PNDXY 6
XX
RESULT 14
ABG35293 standard; Peptide: 21 AA.
AC ABG35293;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human PAR1 type thrombin receptor based peptide #97.
XX
KW PAR1; thrombin receptor; antiinflammatory; cytostatic; human;
KW inflammatory disease; cell proliferative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN JP2002010784-A.
XX
PD 15-JAN-2002.
XX
PF 29-JUN-2000; 2000JP-0196514.
XX
PR 29-JUN-2000; 2000JP-0196514.
XX
PA (TEIJ) TEIJIN LTD.
XX
DR WPI: 2002-321520/36.
XX
PT An inhibitor of cell growth mediated by thrombin used to treat
PT inflammatory and cell proliferative diseases -
XX
PS Example 11; Page 43; 44pp; Japanese.
XX
CC The invention relates to a polypeptide or a compound which can inhibit
CC cell growth caused by thrombin. The polypeptide/compound combines to a
CC specific region of the structure of PAR1 type human thrombin receptor
CC participating to cell growth. Preferably, the compound contains the
CC 52nd to the 56th amino acid sequences at the amino end side of PAR1 type
CC human thrombin receptor ((X4)-Tyr-Glu-Pro-Phe-Trp-(X5) X4, X5 = optional
CC human thrombin receptor ((X4)-Tyr-Glu-Pro-Phe-Trp-(X5) X4, X5 = optional

CC amino acid or peptide sequence). Also included are a modified PAR1 type
CC thrombin receptor gene or its fragment used for obtaining the above
CC polypeptide, a human PAR1 type thrombin receptor protein and its
CC encoding DNA comprising a fully. The polypeptide or the compound is used
CC to treat inflammatory diseases and cell proliferative diseases. The
CC present sequence is a peptide compound of the invention based on the PAR1
CC type thrombin receptor (or a modified version).
XX
SQ Sequence 21 AA;
XX
Query Match 36.0%; Score 18; DB 23; Length 21;
Best Local Similarity 60.0%; Pred. No. 7.5e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 PNXXY 5
DB 2 PNDXY 6
XX
RESULT 15
ABG35295 standard; Peptide: 21 AA.
AC ABG35295;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human PAR1 type thrombin receptor based peptide #99.
XX
KW PAR1; thrombin receptor; antiinflammatory; cytostatic; human;
KW inflammatory disease; cell proliferative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN JP2002010784-A.
XX
PD 15-JAN-2002.
XX
PF 29-JUN-2000; 2000JP-0196514.
XX
PR 29-JUN-2000; 2000JP-0196514.
XX
PA (TEIJ) TEIJIN LTD.
XX
DR WPI: 2002-321520/36.
XX
PT An inhibitor of cell growth mediated by thrombin used to treat
PT inflammatory and cell proliferative diseases -
XX
PS Example 11; Page 21; 44pp; Japanese.
XX
CC The invention relates to a polypeptide or a compound which can inhibit
CC cell growth caused by thrombin. The polypeptide/compound combines to a
CC specific region of the structure of PAR1 type human thrombin receptor
CC participating to cell growth. Preferably, the compound contains the
CC 52nd to the 56th amino acid sequences at the amino end side of PAR1 type
CC human thrombin receptor ((X4)-Tyr-Glu-Pro-Phe-Trp-(X5) X4, X5 = optional
CC amino acid or peptide sequence). Also included are a modified PAR1 type
CC thrombin receptor gene or its fragment used for obtaining the above
CC polypeptide, a human PAR1 type thrombin receptor protein and its
CC encoding DNA comprising a fully. The polypeptide or the compound is used
CC to treat inflammatory diseases and cell proliferative diseases. The
CC present sequence is a peptide compound of the invention based on the PAR1
CC type thrombin receptor (or a modified version).
XX
SQ Sequence 21 AA;
XX
Query Match 36.0%; Score 18; DB 23; Length 21;
Best Local Similarity 60.0%; Pred. No. 7.5e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 PNXXY 5

Db 2 PNDKY 6

RESULT 16
ABG35296
ID ABG35296 standard; Peptide: 21 AA.

AC ABG35296;

DT 15-JUL-2002 (first entry)

DE Human PAR1 type thrombin receptor based peptide #100.

KW PAR1; thrombin receptor; antiinflammatory; cytostatic; human;
inflammatory disease; cell proliferative disease.

OS Homo sapiens.

OS Synthetic.

PN JP2002010784-A.

PD 15-JAN-2002.

PF 29-JUN-2000; 2000JP-0196514.

PR 29-JUN-2000; 2000JP-0196514.

PA (TEIJU) TEIJIN LTD.

DR WPI; 2002-321520/36.

PT An inhibitor of cell growth mediated by thrombin used to treat
inflammatory and cell proliferative diseases -

PS Example 11; Page 43; 44pp; Japanese.

CC The invention relates to a polypeptide or a compound which can inhibit
cell growth caused by thrombin. The polypeptide/compound combines to a
specific region of the structure of PAR1 type human thrombin receptor
participating to cell growth. Preferably, the compound contains the
52nd to the 56th amino acid sequences at the amino end side of PAR1 type
human thrombin receptor ((X4)-Tyr-Glu-Pro-Phe-Trp-(X5) X4, X5 - optional
amino acid or peptide sequence). Also included are a modified PAR1 type
thrombin receptor gene or its fragment used for obtaining the above
polypeptide, a human PAR1 type thrombin receptor protein and its
encoding DNA comprising a fully. The polypeptide or the compound is used
to treat inflammatory diseases and cell proliferative diseases. The
present sequence is a peptide compound of the invention based on the PAR1
type thrombin receptor (or a modified version).

SQ Sequence 21 AA;

Query Match 36.0%; Score 18; DB 23; Length 21;
Best Local Similarity 60.0%; Pred. No. 7.5e+02;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5

Db 2 PNDKY 6

RESULT 17

AAU76681
ID AAU76681 standard; Peptide: 21 AA.

AC AAU76681;

DT 21-MAY-2002 (first entry)

DE Influenza A virus haemagglutinin 3 (H3) antigenic site C variant #3.

KW Haemagglutinin 3; H3; virulence; anti-HIV; human immunodeficiency virus;

KW vaccine; selective advantage; variant; antigenic site; quasiespecies;
variable viral population.

OS Influenza A virus.

PN US6337181-B1.

PD 08-JAN-2002.

PF 21-DEC-1998; 98US-0217293.

PR 21-DEC-1998; 98US-0217293.

PA (STEM/) STEWART J J.

PA (LITW/) LITWIN S.

PI (WATV/) WATTS P.

DR Stewart JJ, Litwin S, Watts P;

DR WPI; 2002-170772/22.

PT Determining viral antigenic protein variants for designing vaccine to
variable viral types and analysing nucleotide sequences of viral
proteins and identifying variants that provide selective advantage to
virus -

PS Example 1; Column 5; 11pp; English.

CC The present invention relates to a new method for determining which
naturally occurring amino acid variants of a protein (subregion) or
antigenic site of a virus are selectively advantageous to the virus.
CC The method of the invention is useful for determining naturally occurring
CC amino acid variants of a protein, protein subregion, or antigenic site of
CC a virus which are selectively advantageous to the virus. The method is
CC useful for identifying appropriate small molecules or other antiviral
CC compounds and for screening broadly neutralising monoclonal antibodies/
CC antiviral compounds. The method is further useful for determining viral
CC antigenic protein variants to be used to construct vaccines designed to
CC immunise against variable viral population (quasiespecies). The present
CC amino acid sequence represents the influenza A virus haemagglutinin 3
CC (H3) antigenic site C peptide variant #3 of the invention.

SQ Sequence 21 AA;

Query Match 36.0%; Score 18; DB 23; Length 21;
Best Local Similarity 60.0%; Pred. No. 7.5e+02;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5

Db 17 PNIGY 21

RESULT 18

ABP46808
ID ABP46808 standard; Peptide: 20 AA.

AC ABP46808;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scfv VH CDR3 SEQ ID 2819.

KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

KW tumour necrosis factor; B cell proliferation; B cell differentiation;

KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;

KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

OS common variable immunodeficiency; acquired immunodeficiency syndrome.

PN WO200202641-A1.

XX 10-JAN-2002.
 PD
 XX
 XX 15-JUN-2001; 2001WO-US19110.
 PF
 XX
 PR 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 DR WPI: 2002-114799/15.
 XX
 PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX
 PS Claim 2; Page 3058; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytosolic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineoplastic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 CC
 SQ Sequence 20 AA;
 XX
 Query Match 34.0%; Score 17; DB 23; Length 20;
 Best Local Similarity 26.7%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 QY 2 NXNXXXXXXXXXX 16
 Db 2 MADYDILGTGPRDY 16
 XX
 RESULT 19
 ID ABP46832
 XX ABP46832 standard; peptide; 20 AA.
 AC ABP46832;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scfv VH CDR3 SEQ ID 2843.
 XX
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antineoplastic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX

PD 10-JAN-2002.
 XX
 XX 15-JUN-2001; 2001WO-US19110.
 PF
 XX
 PR 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 DR WPI: 2002-114799/15.
 XX
 PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
 PT the diagnosis and treatment of cancers and immune disorders -
 XX
 PS Claim 2; Page 3063; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytosolic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineoplastic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 CC
 SQ Sequence 20 AA;
 XX
 Query Match 34.0%; Score 17; DB 23; Length 20;
 Best Local Similarity 25.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
 QY 1 PNXXXXXXXXXX 16
 Db 2 PSEYDILGTGFLPY 17
 XX
 RESULT 20
 ID AAR79996
 XX AAR79996 standard; peptide; 21 AA.
 AC AAR79996;
 XX
 DT 01-MAY-1996 (first entry)
 XX
 DE ARH1 peptide mimotope, mouse CD3-epsilon.
 XX
 KW Signal transduction; src-family thymidine kinase; lipid kinase;
 KW tyrosine kinase; adaptor; inhibition; regulation; immunodeficiency;
 KW allergy; inflammation; cancer; autoimmune disease; Epstein-Barr virus;
 KW immunoproliferative disease; bovine leukaemia virus; EBV; BLV;
 KW chronic fatigue syndrome; infectious mononucleosis.
 XX
 OS Mus sp.
 XX
 PN WO9524915-A1.
 XX
 PD 21-SEP-1995.
 XX

OS Synthetic.
 XX
 PN WO200226781-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 26-SEP-2001; 2001WO-US30289.
 XX
 PR 26-SEP-2000; 2000US-235353P.
 PR 23-MAR-2001; 2001US-278540P.
 XX
 PA (GETH) GENEWTECH INC.
 XX
 PL Lowman HB, Reynolds ME, Nakamura GR, Starovasnik MA;
 DR WPI; 2002-444016/47.
 XX
 PT A peptide useful for treating a IGE-mediated disease or disorder in a
 PT host e.g. allergic rhinitis, asthma, which competes with immunoglobulin
 PT E for binding to high affinity IGE receptor in an in vitro assay
 XX
 PS Example 8; Fig 1; 328pp; English.
 XX
 CC The invention relates to a peptide which competes with immunoglobulin
 CC (Ig) E 134 comprising a sequence (SI), for binding the high affinity IGE
 CC receptor (FcεpsilonRI) in an in vitro assay and having a formula given in
 CC the specification. Also included are a fusion protein comprising the
 CC peptide, a pharmaceutical composition (C) comprising the peptide,
 CC designing a compound that mimics the three-dimensional surface
 CC structure of the peptide, a compound with a solvent accessible surface
 CC that mimics the solvent accessible surface defined by the side chains of
 CC residues (R) Pro4, Phe6, Pro16, Cys3, Cys7, Cys15 and Cys19 of IGE134,
 CC selecting a peptide mimetic which binds to FcεpsilonRI and blocks
 CC binding of IGE and a peptide mimetic which mimics the coordinates of
 CC IGE134 residues (R). (C) is useful for inhibiting the binding of IGE to
 CC high affinity IGE receptor (FcεpsilonRI). Peptides of the formula given
 CC in the specification are useful for inhibiting the binding of an IGE to
 CC molecule which blocks the interaction of IGE with high affinity IGE
 CC receptor. The peptide is also useful for inhibiting the activation of
 CC high affinity IGE receptor. The peptide is useful for treating an IGE-
 CC mediated disease or disorder in a host. (C) is useful in research,
 CC diagnostic, therapeutic and prophylactic methods. The peptide is also
 CC useful for inhibiting IGE-mediated or associated processes such as IGE-
 CC dependent activation and degranulation of mast cells and basophils, as
 CC well as consequent release of inflammatory mediators such as histamine.
 CC (C) is useful for treating allergic rhinitis, asthma (e.g. allergic
 CC asthma), atopic dermatitis, urticaria-angioedema, parasitic infection,
 CC IGE myeloma, immune-related disorders, inflammatory diseases, diabetes
 CC mellitus, IGE-mediated gastrointestinal inflammatory disease, immune
 CC rejection of grafts, reperfusion injury, stroke, myocardial infarction,
 CC atherosclerosis, acute lung injury, hemorrhagic shock, burn, septic
 CC shock, acute tubular necrosis, endometritis, degenerative joint disease
 CC and pancreatitis. The present sequence is a peptide of the invention
 CC expressed from a phage display library.
 XX
 SQ Sequence 21 AA:
 Query Match 34.0%; Score 17; DB 23; Length 21;
 Best Local Similarity 60.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AC ABG66416;
 XX
 DT 30-AUG-2002 (first entry)
 XX
 DE IGE Fcεpsilon RI binding peptide IGE120 #59.
 XX
 KW IGE receptor; immunoglobulin; FcεpsilonRI; antagonist; phage display;
 KW protein co-ordinate data; IGE-mediated disease; allergic rhinitis;
 KW asthma; allergic asthma; atopic dermatitis; urticaria-angioedema;
 KW parasitic infection; IGE myeloma; immune-related disorder;
 KW inflammatory disorder; diabetes mellitus; reperfusion injury; stroke;
 KW IGE-mediated gastrointestinal inflammatory disease; burn;
 KW immune rejection of graft; myocardial infarction; atherosclerosis;
 KW acute lung injury; hemorrhagic shock; septic shock;
 KW acute tubular necrosis; endometritis; degenerative joint disease;
 KW pancreatitis.
 XX
 OS Synthetic.
 XX
 PN WO200226781-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 26-SEP-2001; 2001WO-US30289.
 XX
 PR 26-SEP-2000; 2000US-235353P.
 PR 23-MAR-2001; 2001US-278540P.
 XX
 PA (GETH) GENEWTECH INC.
 XX
 PL Lowman HB, Reynolds ME, Nakamura GR, Starovasnik MA;
 DR WPI; 2002-444016/47.
 XX
 PT A peptide useful for treating a IGE-mediated disease or disorder in a
 PT host e.g. allergic rhinitis, asthma, which competes with immunoglobulin
 PT E for binding to high affinity IGE receptor in an in vitro assay
 XX
 PS Example 8; Fig 2; 328pp; English.
 XX
 CC The invention relates to a peptide which competes with immunoglobulin
 CC (Ig) E 134 comprising a sequence (SI), for binding the high affinity IGE
 CC receptor (FcεpsilonRI) in an in vitro assay and having a formula given in
 CC the specification. Also included are a fusion protein comprising the
 CC peptide, a pharmaceutical composition (C) comprising the peptide,
 CC designing a compound that mimics the three-dimensional surface
 CC structure of the peptide, a compound with a solvent accessible surface
 CC that mimics the solvent accessible surface defined by the side chains of
 CC residues (R) Pro4, Phe6, Pro16, Cys3, Cys7, Cys15 and Cys19 of IGE134,
 CC selecting a peptide mimetic which binds to FcεpsilonRI and blocks
 CC binding of IGE and a peptide mimetic which mimics the coordinates of
 CC IGE134 residues (R). (C) is useful for inhibiting the binding of IGE to
 CC high affinity IGE receptor (FcεpsilonRI). Peptides of the formula given
 CC in the specification are useful for inhibiting the binding of an IGE to
 CC molecule which blocks the interaction of IGE with high affinity IGE
 CC receptor. The peptide is also useful for inhibiting the activation of
 CC high affinity IGE receptor. The peptide is useful for treating an IGE-
 CC mediated disease or disorder in a host. (C) is useful in research,
 CC diagnostic, therapeutic and prophylactic methods. The peptide is also
 CC useful for inhibiting IGE-mediated or associated processes such as IGE-
 CC dependent activation and degranulation of mast cells and basophils, as
 CC well as consequent release of inflammatory mediators such as histamine.
 CC (C) is useful for treating allergic rhinitis, asthma (e.g. allergic
 CC asthma), atopic dermatitis, urticaria-angioedema, parasitic infection,
 CC IGE myeloma, immune-related disorders, inflammatory diseases, diabetes
 CC mellitus, IGE-mediated gastrointestinal inflammatory disease, immune
 CC rejection of grafts, reperfusion injury, stroke, myocardial infarction,
 CC atherosclerosis, acute lung injury, hemorrhagic shock, burn, septic
 CC shock, acute tubular necrosis, endometritis, degenerative joint disease
 CC and pancreatitis. The present sequence is a peptide of the invention
 CC expressed from a phage display library.

RESULT 23
 ABG66416,
 ID ABG66416 standard; Peptide: 21 AA.
 XX

```

XX Sequence 21 AA:
Query Match 34.0%; Score 17; DB 23; Length 21;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
DB 16 PNMXY 20

RESULT 24
AAW78202
ID AAW78202 standard; Protein: 20 AA.
AC AAW78202;
XX
XX 13-APR-1999 (first entry)
DE Human secreted protein encoded by gene 77 clone HMSPD68.
XX
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
XX developmental abnormality; foetal deficiency; blood; allergy; renal;
XX immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
XX cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 20 /label= unknown
XX
XX WO9856804-A1.
XX
PD 17-DEC-1998.
XX
XX 11-JUN-1998; 98WO-US12125.
XX
XX 02-OCT-1997; 97US-0061060.
XX PR 13-JUN-1997; 97US-0049547.
XX PR 13-JUN-1997; 97US-0049548.
XX PR 13-JUN-1997; 97US-0049549.
XX PR 13-JUN-1997; 97US-0049550.
XX PR 13-JUN-1997; 97US-0049606.
XX PR 13-JUN-1997; 97US-0049607.
XX PR 13-JUN-1997; 97US-0049608.
XX PR 13-JUN-1997; 97US-0049609.
XX PR 13-JUN-1997; 97US-0049610.
XX PR 13-JUN-1997; 97US-0049611.
XX PR 13-JUN-1997; 97US-0050566.
XX PR 13-JUN-1997; 97US-0050901.
XX PR 13-JUN-1997; 97US-0052989.
XX PR 08-JUL-1997; 97US-0051919.
XX PR 18-AUG-1997; 97US-0055984.
XX PR 12-SEP-1997; 97US-0058665.
XX PR 12-SEP-1997; 97US-0058668.
XX PR 12-SEP-1997; 97US-0058669.
XX PR 12-SEP-1997; 97US-0058750.
XX PR 12-SEP-1997; 97US-0058971.
XX PR 12-SEP-1997; 97US-0058972.
XX PR 12-SEP-1997; 97US-0058975.
XX PR 02-OCT-1997; 97US-0060834.
XX PR 02-OCT-1997; 97US-0060844.
XX PR 02-OCT-1997; 97US-0060865.
XX PR 02-OCT-1997; 97US-0061059.
XX
XX (HUMA-) HUMAN GENOME SCI INC.

```

```

XX
PI Brewer LA, Ebner R, Ferrie AM, Feng P, Greene JM, Lafleur DM;
PI Moore PA, M J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P;
PI Yu GL;
XX
XX WPI; 1999-080881/07.
XX
XX N-PSDB; AAX04387.
XX
XX
XX New isolated human genes and the secreted polypeptides they encode -
XX useful for diagnosis and treatment of e.g. cancers, neurological
XX disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 11; Page 308; 380pp; English.
XX
XX This sequence represents a secreted human protein encoded by the gene
XX clone detailed in the descriptor line. The gene can be used to generate
XX fusion proteins by linking to the gene to a human immunoglobulin Fc
XX portion (e.g. AAX04302) for increasing the stability of the fused
XX protein as compared to the human protein only.
XX The invention relates to 86 novel genes and their fragments (nucleic
XX acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225)
XX which are useful for preventing, treating or ameliorating medical
XX conditions e.g. by protein or gene therapy. Also, pathological
XX conditions can be diagnosed by determining the amount of the new
XX polypeptides in a sample or by determining the presence of mutations in
XX the new polynucleotides. Specific uses are described for each of the 86
XX polynucleotides, based on which tissues they are most highly expressed in
XX (see AAX04311 for described uses).
XX
XX
XX Sequence 20 AA:

```

```

Query Match 32.0%; Score 16; DB 20; Length 20;
Best Local Similarity 27.3%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

QY 1 PNXYYXXXXXY 11
DB 7 PKSFYIKLSY 17

```

```

RESULT 25
AAU02715
ID AAU02715 standard; Peptide: 20 AA.
XX
XX AAU02715;
XX
XX 29-AUG-2001 (first entry)
XX
XX CDR region of anti-adipocyte antibody heavy chain, FAT 82.
XX
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX heart disease; complementarity determining region; CDR.
XX
XX Homo sapiens.
XX
XX WO200127279-A1.
XX
XX 19-APR-2001.
XX
XX 11-OCT-2000; 2000WO-GB03900.
XX
XX 12-OCT-1999; 99US-0158812.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Edwards BM, Main SH, Vaughan TJ;
XX
XX WPI; 2001-282031/29.
XX
XX N-PSDB; AAS03494.
XX
XX Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity
XX related diseases -

```

XX Example 7: Page 78; 182pp; English.

CC AA02501-AA02635, and AA02641-AA02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light
CC chain, and heavy chain complementarily determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease.

CC Sequence 20 AA;

Query Match 32.0%; Score 16; DB 22; Length 20;
Best Local Similarity 27.3%; Pred. NO. 2.3e+03;
Matches 3; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 PNXXYXXXXXX 11
Db 3 PYYYYSSGGY 13

RESULT 26

ABP46758
ID ABP46758 standard; peptide: 21 AA.

AC ABP46758;

DT 19-AUG-2002 (first entry)

DE Human BlyS binding scFv VH CDR3 SEQ ID 2769.

XX BlyS: B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US19110.

PR 16-JUN-2000; 2000US-212210P.

PR 17-OCT-2000; 2000US-240816P.

PR 16-MAR-2001; 2001US-276248P.

PR 21-MAR-2001; 2001US-277379P.

PR 25-MAY-2001; 2001US-293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

DR WPI; 2002-114799/15.

XX Antibodies against B lymphocyte stimulating polypeptides, useful for

PT the diagnosis and treatment of cancers and immune disorders -

PS Claim 2: Page 3048; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
CC and so may be used to detect and quantitate the presence of BlyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BlyS. They may also be
CC administered to treat diseases associated with aberrant BlyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method
CC of the invention.

CC Sequence 21 AA;

Query Match 33.0%; Score 16; DB 23; Length 21;
Best Local Similarity 26.7%; Pred. NO. 2.4e+03;
Matches 4; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2 NXKXXXXXXKX 16
Db 1 NGYDILGYIMDY 15

RESULT 27

AAE20075
ID AAE20075 standard; peptide: 21 AA.

AC AAE20075;

DT 18-JUN-2002 (first entry)

DE Complement C1s exosite binding moiety, peptide #3.

XX Complement C1s: therapeutic; adult respiratory distress syndrome; stroke;
KW preservative; ischemia-reperfusion injury; myocardial infarct; sepsis;
KW hyperacute rejection; rheumatoid arthritis; burn; wound healing; asthma;
KW systemic lupus erythematosus; SLE; haemolytic anaemia; serum sickness;
XX restenosis; myasthenia gravis.

XX Unidentified.

OS Unidentified.

PN Key

FT Modified-site 3 Location/Qualifiers

FT Modified-site 4 /label= Asp, Glu

FT Modified-site 6 /label= Asp, Glu

FT Modified-site 7 /note= "Sulphated Phe"

FT Modified-site 8 /note= "Sulphated Tyr"

FT Modified-site 9 /note= "2-sulphotyrosine"

FT Modified-site 10 /label= Asp, Glu

FT Modified-site 12 /label= Asp, Glu

FT Modified-site 13 /note= "Sulphated Phe"

FT Modified-site 14 /note= "Sulphated Tyr"

FT Modified-site 15 /note= "2-sulphotyrosine"

FT Modified-site 17 /label= Asp, Glu

FT	Modified-site	/note= "Sulphated Phe"
FT	18	
FT	Modified-site	/note= "Sulphated Tyr"
FT	19	
FT	Modified-site	/note= "2-sulphotyrosine"
FT	20	
FT	Misc-difference	/label= Asp, Glu
FT	21	
FT	/label= Asp, Glu	
FT	/note= "Optionally absent"	
PN	WO200198365-A2.	
XX		
XX	27-DEC-2001.	
XX		
PF	18-JUN-2001; 2001WO-US19405.	
XX		
PR	21-JUN-2000; 2000US-212998P.	
XX		
PA	(ZYMO) ZYMOGENETICS INC.	
XX		
PI	West RR, Sheppard PO, Fox BA;	
DR	WPI; 2002-241177/29.	
XX		
PT	New complement C1s inhibitor polypeptides for treating diseases in	
PT	which complement activation has been shown to occur, e.g. adult	
PT	respiratory distress syndrome, ischemia-reperfusion injury, asthma, or	
PT	sepsis	
XX		
PS	Claim 16; Page 52; 99pp; English.	
XX		
CC	The invention relates to a polypeptide that inhibits complement C1s. The	
CC	inhibitory peptides are useful as therapeutic agents, as preservatives	
CC	in blood samples, and in affinity purification procedures to isolate C1s.	
CC	Molecules that inhibit complement may be used for treating diseases	
CC	in which complement activation has been shown to occur, e.g., adult	
CC	respiratory distress syndrome, ischemia-reperfusion injury (myocardial	
CC	infarct, stroke), hyperacute rejection, sepsis, burns, wound healing,	
CC	asthma, restenosis, rheumatoid arthritis, systemic lupus erythematosus,	
CC	serum sickness, haemolytic anaemias, or myasthenia gravis. The present	
CC	peptide sequence is complement C1s exosite binding moiety.	
XX		
SO	Sequence 21 AA;	
QY	2 NXXYXXXXXXXY 16	
DB	2 NXXYFYXXYFYXX 16	
RESULT 28		
ID	AAE20125	
XX	AAE20125 standard; peptide: 21 AA.	
XX		
XX	AAE20125;	
DE	18-JUN-2002 (first entry)	
XX		
XX	Complement C1s inhibitor peptide #2 alternative version.	
XX		
XX	Complement C1s; therapeutic; adult respiratory distress syndrome; stroke;	
XX	preservative; ischemia-reperfusion injury; myocardial infarct; sepsis;	
XX	hyperacute rejection; rheumatoid arthritis; burn; wound healing; asthma;	
XX	systemic lupus erythematosus; STE; haemolytic anaemia; serum sickness;	
XX	restenosis; myasthenia gravis.	
XX		
XX	Unidentified.	
XX		
XX		
XX	Key	Location/Qualifiers

FT	Modified-site	1	/label= Ala, Pro
FT	Modified-site	3	/label= Asp, Glu
FT	Modified-site	4	/label= Asp, Glu
FT	Modified-site	6	/note= "Sulphated Phe"
FT	Modified-site	7	/note= "Sulphated Tyr"
FT	Modified-site	8	/note= "2-sulphotyrosine"
FT	Modified-site	9	/label= Asp, Glu
FT	Modified-site	10	/label= Asp, Glu
FT	Modified-site	12	/note= "Sulphated Phe"
FT	Modified-site	13	/note= "Sulphated Tyr"
FT	Modified-site	14	/note= "2-sulphotyrosine"
FT	Modified-site	15	/label= Asp, Glu
FT	Modified-site	17	/note= "Sulphated Phe"
FT	Modified-site	18	/note= "Sulphated Tyr"
FT	Modified-site	18	/note= "2-sulphotyrosine"
FT	Modified-site	20	/label= Asp, Glu
FT	Misc-difference	21	/label= Asp, Glu
FT	Misc-difference	21	/note= "Optionally absent"
PN	WO200198365-A2.		
PD	27-DEC-2001.		
XX			
XX	18-JUN-2001; 2001WO-US19405.		
XX			
PR	21-JUN-2000; 2000US-212988P.		
XX			
PA	(ZYMO) ZYMOGENETICS INC.		
XX			
PI	West RR, Sheppard PO, Fox BA;		
DR	WPI; 2002-241177/29.		
XX			
PT	New complement C1s inhibitor polypeptides for treating diseases in		
PT	which complement activation has been shown to occur, e.g. adult		
PT	respiratory distress syndrome, ischemia-reperfusion injury, asthma, or		
XX	sepsis		
PS	Claim 5; Page 186; 99pp; English.		
XX			
CC	The invention relates to a polypeptide that inhibits complement C1s. The		
CC	inhibitory peptides are useful as therapeutic agents, as preservatives		
CC	in blood samples, and in affinity purification procedures to isolate C1s		
CC	molecules that inhibit complement may be used for treating diseases		
CC	in which complement activation has been shown to occur, e.g., adult		
CC	respiratory distress syndrome, ischemia-reperfusion injury (myocardial		
CC	infarct, stroke), hyperacute rejection, sepsis, burns, wound healing,		
CC	asthma, restenosis), rheumatoid arthritis, systemic lupus erythematosus,		
CC	serum sickness, hemolytic anaemias, or myasthenia gravis. The present		
CC	sequence is an alternative version of complement C1s inhibitor peptide.		
CC	Note: This sequence is an alternative version of complement inhibitor		
CC	peptide referred as SEQ ID No: 126 (AAE20073) in page 49 of the		
CC	specification (N00228).		
XX			
XX	Sequence 21 AA;		

Query Match 32.0%; Score 16; DB 23; Length 21;
 Best Local Similarity 60.0%; Pred. No. 2.4e+03;
 Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 NXXXXXXYYXXYY 16
 |||| ||||
 2 NXXYYXXYYXXYY 16

RESULT 29

AAR33444
 ID AAR33444 standard; peptide; 20 AA.

AC AAR33444;

DT 30-JUN-1993 (first entry)

DE HCV NS5 fragment encoded by PHCV45 clone.

KM Monoclonal antibody; hybridoma; E.coli; diagnosis.

OS Hepatitis C virus.

PN WO9304084-A.

PD 04-MAR-1993.

PF 21-AUG-1992; 92WO-US06965.

PR 21-AUG-1991; 91US-0748563.

PA (ABB0) ABBOTT LAB.

PI Dailey SH, Desai SM, Devare SG, Johnson JE, Mehta SU;

DR WPI; 1993-093937/11.

PT Monoclonal antibodies to hepatitis C virus NS5 proteins - used in
 PT diagnosing hepatitis C infections and differentiation studies

PS Disclosure; Page 21; 38pp; English.

CC The sequence is that of an E. coli derived fragment of Hepatitis C
 CC virus NS5. The sequence may be used to raise monoclonal antibodies
 CC which specifically bind HCV NS5 antigen and to produce the hybridoma
 CC cell lines ATCC HB 10854 and HB 10855.
 CC See also AAR33441-3.

SO Sequence 20 AA;

Query Match 30.0%; Score 15; DB 14; Length 20;
 Best Local Similarity 40.0%; Pred. No. 4.1e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
 ||||
 5 PNYTF 9

RESULT 30

AAR84491
 ID AAR84491 standard; peptide; 20 AA.

AC AAR84491;

DT 06-JAN-1997 (first entry)

DE Hepatitis C virus T-cell epitope peptide NS1-23 (residues 583-602).

KM Hepatitis C virus; HCV; immunogen; non-structural region;
 KM immunodominant; T cell epitope; vaccine.

OS Hepatitis C virus.

XX WO9512677-A2.

PD 11-MAY-1995.

PF 28-OCT-1994; 94WO-EP03555.

PR 04-NOV-1993; 93EP-0402718.

PA (INNO-) INNOGENETICS NV.

PI Deleys R, Leroux-Roels G, Maertens G;

DR WPI; 1995-193822/25.

PT Hepatitis C Virus immunogenic polypeptide cont. a T-cell
 PT stimulating epitope - from core, E1, E2 and NS3 regions, useful in
 PT production of vaccines, therapeutic agents, etc.

PS Claim 26; Page 71; 105pp; English.

CC The present sequence is a specifically claimed example of a
 CC T-cell epitope-containing peptide derived from hepatitis C virus.

SO Sequence 20 AA;

Query Match 30.0%; Score 15; DB 16; Length 20;
 Best Local Similarity 40.0%; Pred. No. 4.1e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
 ||||
 8 PDATY 12

RESULT 31

AAR91009
 ID AAR91009 standard; peptide; 20 AA.

AC AAR91009;

DT 25-SEP-1996 (first entry)

DE HCV E2 peptide E2-23 for competition studies.

KM HCV; E1; E2; disulphide bond cleavage; envelope protein; vaccine; human;
 KM serotype; reversed phase hybridisation assay; genotype; antigen; sera.

OS Synthetic.

PN WO9604385-A2.

PD 15-FEB-1996.

PF 31-JUL-1995; 95WO-EP03031.

PR 29-JUL-1994; 94EP-0870132.

PA (INNO-) INNOGENETICS NV.

PI Bosman F, Buyse M, De Martynoff G, Maertens G;

DR WPI; 1996-129401/13.

PT Purifying recombinant hepatitis C virus (HCV) E1 and E2 envelope
 PT proteins - in presence of disulphide bond cleavage agent, to
 PT produce proteins suitable for direct use in vaccines or diagnostic
 PT assays of HCV

PS Claim 29; Page 67; 146pp; English.

CC AAR90965-R90980 and AAR90995-R91015 represent synthetic hepatitis C
 CC virus (HCV) E1 and E2 peptides used in competition studies. This

CC sequence represents a synthetic E2 peptide, and corresponds to residues
CC 583-602 of the E2 protein sequence. These sequences are useful for in
CC vitro monitoring of HCV disease, or prognosis of the response to
CC interferon treatment of patients suffering from HCV infection. These
CC sequences compete with the proteins produced by AAT12704-t12709 and
CC AAT12961-t12974, which are included in vectors for the production of
CC recombinant E1, E2, and E1/E2. The recombinant proteins can then be
CC isolated and purified by carrying out a disulphide bond cleavage, or a
CC reduction step with a disulphide bond cleavage agent, after lysis of
CC recombinant host cells. The constructs containing the purified HCV
CC envelope proteins can be used for vaccinating humans against HCV, for in
CC vitro detection of HCV antibodies in a sample, and in a serotyping assay
CC for detecting one or more serological types of HCV present in a
CC biological sample. The constructs can also be immobilised on a solid
CC substrate and incorporated into a reversed phase hybridisation assay for
CC determining the presence or the genotype of HCV. The new purification
CC method preserves the conformation of the recombinantly expressed E1, E2
CC and E1/E2, and eliminates contaminating proteins. Antigens isolated
CC by this method are more reactive with human sera than those isolated
CC by known techniques.

SQ Sequence 20 AA:

Query Match 30.0%; Score 15; DB 17; Length 20;
Best Local Similarity 40.0%; Pred. No. 4.1e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
I: |
Db 8 PDATY 12

RESULT 32

AA67694 standard; peptide; 20 AA.

AA67694;

23-MAR-2000 (first entry)

Peptide #94 for detecting hepatitis C virus infection.

Hepatitis C virus; HCV; increased structural stability; E1 region;
KM diagnostic antigen.

OS Hepatitis C virus.

XX MO9962945-A2.

XX 09-DEC-1999.

XX 04-JUN-1999; 99MO-US12446.

XX 05-JUN-1998; 98US-0088229.

PR 01-SEP-1998; 98US-0098705.

PR 15-SEP-1998; 98US-0100422.

PR 28-JAN-1999; 99MO-US01726.

(PEPT-) PEPTIDE SOLUTIONS INC.

XX Chowdhury MA, Bernstein D, Molsenbocker MA;

XX MPI; 2000-086953/07.

XX Improving properties of peptides for use as diagnostic antigens or for
XX preventing or treating infections -

XX Claim 55; Page 66; 83pp; English.

CC This is a peptide from the immunoreactive region of the E1 region of
CC hepatitis C virus (HCV). The peptide is useful for detecting HCV
CC infection. The invention relates to peptides derived from HCV and also
CC HIV-1 which have been modified for use as diagnostic antigens in the

CC treatment or prevention of infection. The structural stability of the
CC peptides can be increased in four different ways; through the replacement
CC of a hydrophobic amino acid with a less hydrophobic amino acid; through
CC an increase in the amount of secondary structure (i.e. alpha helix) in
CC the peptide; through the removal of a positive charge from the peptide,
CC or through the constraint of the epitopic sequence via the formation of a
CC covalent crosslink. Modified peptides of the invention are used to detect
CC infectious agents specifically HCV. Other detectable agents include HIV-1
CC Group O viruses; human T-cell lymphotropic virus-1 or -II; and the
CC causative agent of syphilis. The peptides can be used for prevention or
CC treatment of infections (e.g. as vaccines, or where expressed from a
CC transgene). More generally almost any peptide can be similarly modified,
CC e.g. cytokines or interferons; major histocompatibility complex antigens;
CC hormones; growth factors; tumour markers or suppressors, or antigens from
CC many other pathogens.

SQ Sequence 20 AA:

Query Match 30.0%; Score 15; DB 21; Length 20;
Best Local Similarity 27.3%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 PNXXYXXXXXX 11
I: |
Db 2 PNSSIYETDY 12

RESULT 33

AA67767 standard; peptide; 20 AA.

AA67767;

23-MAR-2000 (first entry)

Peptide #167 for detecting hepatitis C virus infection.

Hepatitis C virus; HCV; increased structural stability; E1 region;
KM diagnostic antigen.

XX Synthetic.

XX MO9962945-A2.

XX 09-DEC-1999.

XX 04-JUN-1999; 99MO-US12446.

XX 05-JUN-1998; 98US-0088229.

PR 01-SEP-1998; 98US-0098705.

PR 15-SEP-1998; 98US-0100422.

PR 28-JAN-1999; 99MO-US01726.

(PEPT-) PEPTIDE SOLUTIONS INC.

XX Chowdhury MA, Bernstein D, Molsenbocker MA;

XX MPI; 2000-086953/07.

XX Improving properties of peptides for use as diagnostic antigens or for
XX preventing or treating infections -

XX Claim 55; Page 71; 83pp; English.

CC This is a peptide related to the immunoreactive region of the E1 region
CC of hepatitis C virus (HCV). The peptide is useful for detecting HCV
CC infection. The invention relates to peptides derived from HCV and also
CC HIV-1 which have been modified for use as diagnostic antigens in the
CC treatment or prevention of infection. The structural stability of the
CC peptide can be increased in four different ways; through the replacement
CC of a hydrophobic amino acid with a less hydrophobic amino acid; through
CC an increase in the amount of secondary structure (i.e. alpha helix) in
CC the peptide; through the removal of a positive charge from the peptide,

CC or through the constraint of the epitopic sequence via the formation of a
CC covalent crosslink. Modified peptides of the invention are used to detect
CC infectious agents specifically HCV. Other detectable agents include HIV-1
CC Group O viruses; human T-cell lymphotropic virus I or II; and the
CC causative agent of syphilis. The peptides can be used for prevention or
CC treatment of infections (e.g. as vaccines, or where expressed from a
CC transgene). More generally almost any peptide can be similarly modified,
CC e.g. cytokines or interferons; major histocompatibility complex antigens;
CC hormones; growth factors; tumour markers or suppressors, or antigens from
CC many other pathogens.

SQ Sequence 20 AA:

Query Match 30.0%; Score 15; DB 21; Length 20;
Best Local Similarity 27.3%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 PNXXXXXXXX 11
11
DB 2 PNSSIVETPDY 12

RESULT 34

AAB66943
ID AAB66943 standard; Peptide: 20 AA.

AC AAB66943;

DT 17-APR-2001 (first entry)

DE RSV M2 ORF2 fragment #2.

XX Immunostimulant; respiratory general; antiinflammatory; vaccine;
KW gene therapy; transcription factor; M2-2; pneumonia;
KM lower respiratory tract disease; bronchiolitis.

OS Human respiratory syncytial virus.

PN W0200104321-A1.

XX 18-JAN-2001.

PF 07-JUL-2000; 2000WO-US18534.

PR 09-JUL-1999; 99US-0143097.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Collins PL, Murphy BR, Bermingham A;

DR WPI; 2001-103086/11.

DR N-PSDB; AAF55896.

XX Isolated infectious recombinant respiratory syncytial virus (RSV) has a
PT modified genome and is used as a noninfectious subunit vaccine and for
PT the production of viral proteins in cell culture -

PS Example 1; Page 20; 124pp; English.

XX The present invention relates to an infectious recombinant respiratory
CC syncytial virus (RSV) which has a modification in the genome/antigenome
CC of the second translational open reading frame encoded by the M2 gene (M2
CC ORF2). The M2 gene encodes transcription/replication regulatory factor
CC response to RSV in a vaccinated host. The immune response is protective
CC against serious lower respiratory tract disease e.g. pneumonia and
CC bronchiolitis, when the individual is subsequently infected with wild
CC type RSV. The M2 ORF2 deletion or knockout mutant can also be used as a
CC vector for transient gene therapy of the respiratory tract. The present
CC sequence is a peptide fragment encoded by the RSV M2 ORF, which was used
XX in the present invention.

SQ Sequence , 20 AA:

Query Match 30.0%; Score 15; DB 22; Length 20;
Best Local Similarity 40.0%; Pred. No. 4.1e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
11
DB 6 PNOTF 10

RESULT 35

AAB55825
ID AAB55825 standard; Peptide: 20 AA.

AC AAB55825;

DT 07-MAR-2001 (first entry)

DE PL peptide #36.

XX Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation;
KW allergy; asthma; multiple sclerosis; cancer; infection.

OS Synthetic.

PN W0200069896-A2;

XX 23-NOV-2000.

PF 12-MAY-2000; 2000WO-US13161.

PR 14-MAY-1999; 99US-0134114.

PR 14-MAY-1999; 99US-0134117.

PR 14-MAY-1999; 99US-0134118.

PR 21-OCT-1999; 99US-0160860.

PR 29-OCT-1999; 99US-0162498.

PR 13-DEC-1999; 99US-0170453.

PR 14-JAN-2000; 2000US-0176195.

PR 14-FEB-2000; 2000US-0182296.

PR 11-APR-2000; 2000US-0196460.

PR 11-APR-2000; 2000US-0196527.

(ARBO-) ARBOR VITA CORP.

PA Lu PS;

DR WPI; 2001-080245/09.

XX Modulating a biological function of an endothelial cell or
PT hematopoietic cell; useful for treating autoimmune diseases and
PT infectious diseases, by administering an antagonist that inhibits
PT binding between a PDZ protein and a PL protein -

PS Disclosure; Page 53; 14pp; English.

XX The present invention relates to a new method for modulating a
CC biological function of an endothelial cell or hematopoietic cell. The
CC method involves introducing into a cell, an antagonist that inhibits
CC binding between a PDZ protein and a PL protein. The inhibitor is used
CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune
CC disease. It may also be used to prevent transplantation rejection of
CC of inflamed organ transplant. The method may also be used in the treatment
CC of inflammation, allergy, inflammatory bowel diseases, ulcerative
CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, autoimmune
CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,
CC graft rejection, transplantation rejection), atherosclerosis, cancers,
CC infectious diseases, ischemia, vasculitis and Crohn's disease.

SQ Sequence 20 AA:

Query Match 30.0%; Score 15; DB 22; Length 20;
Best Local Similarity 40.0%; Pred. No. 4.1e+03;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 PNXXY 5
 | : |
 Db 3 PSSSY 7

RESULT 36
 AAB57687
 ID AAB57687 standard; Peptide: 20 AA.

AC AAB57687;

DF 12-MAR-2001 (first entry)

DE CC CKR-4 PL peptide.

XX Endothelial cell; haematopoietic cell; PDZ domain protein;
 KW PL domain protein; leukocyte activation; synapse formation;
 KW transmembrane neurotransmitter receptor; autoimmune disease;
 KW transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
 KW ischaemia; vasculitis; Crohn's disease.

OS Homo sapiens.

PN WO200069897-A2.

PD 23-NOV-2000.

PF 12-MAY-2000; 2000WO-US13166.

XX 14-MAY-1999; 99US-0134114.
 PR 14-MAY-1999; 99US-0134117.
 PR 14-MAY-1999; 99US-0134118.
 PR 21-OCT-1999; 99US-0160860.
 PR 29-OCT-1999; 99US-0162498.
 PR 13-DEC-1999; 99US-0170453.
 PR 14-JAN-2000; 2000US-0176195.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.

XX (ARBO-) ARBOR VITA CORP.

XX Lu PS;

DR WPI; 2001-025003/03.

XX New inhibitors of binding of a PDZ protein and PL protein for
 PT inhibiting T cell-mediated response by haematopoietic cells, or for
 PT treating diseases characterized by inflammatory and humoral immune
 PT responses, e.g. inflammation, cancer

XX Disclosure: Page 51; 139pp; English.

XX The present invention relates to a method for modulating a biological
 CC function of an endothelial cell or haematopoietic cell, comprises
 CC introducing into a cell an antagonist that inhibits binding between a
 CC PDZ domain protein and a PL domain protein to result in inhibition of
 CC leukocyte activation. The present sequence is a PL peptide. PDZ domains
 CC of proteins are named after three prototypical proteins: PSD95,
 CC Drosophila large disc protein and Zonula Occludin 1 protein. PDZ domain
 CC proteins are involved in synapse formation by organising transmembrane
 CC neurotransmitter receptors through intracellular interactions. The
 CC inhibitors identified by the present invention can be used to treat a
 CC disease mediated by haematopoietic cells, e.g. autoimmune disease,
 CC inflammation, allergy (e.g. drug allergies), inflammatory bowel diseases,
 CC ulcerative colitis, ileitis, psoriasis, respiratory allergic diseases
 CC (e.g. asthma), atopic dermatitis, autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, insulin-dependent diabetes, Hashimoto
 CC thyroiditis, osteoarthritis), atherosclerosis, cancers, infectious

CC diseases (e.g. viral infection), ischaemia, vasculitis and Crohn's
 CC disease. The inhibitors can also be used to prevent transplantation
 CC rejection of a solid organ transplant.

SO Sequence 20 AA:

Query Match 30.0%; Score 15; DB 22; Length 20;
 Best Local Similarity 40.0%; Pred. No. 4.1e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
 | : |
 Db 3 PSSSY 7

RESULT 37
 AAB58097
 ID AAB58097 standard; Peptide: 20 AA.

AC AAB58097;

DF 12-MAR-2001 (first entry)

DE CC CKR-4 PL peptide.

XX Endothelial cell; haematopoietic cell; PDZ domain protein;
 KW PL domain protein; leukocyte activation; synapse formation;
 KW transmembrane neurotransmitter receptor; autoimmune disease;
 KW transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
 KW ischaemia; vasculitis; Crohn's disease.

OS Homo sapiens.

PN WO200069898-A2.

PD 23-NOV-2000.

XX 12-MAY-2000; 2000WO-US13205.
 XX 14-MAY-1999; 99US-0134114.
 PR 14-MAY-1999; 99US-0134117.
 PR 14-MAY-1999; 99US-0134118.
 PR 21-OCT-1999; 99US-0160860.
 PR 29-OCT-1999; 99US-0162498.
 PR 13-DEC-1999; 99US-0170453.
 PR 14-JAN-2000; 2000US-0176195.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.

XX (ARBO-) ARBOR VITA CORP.

XX Lu PS;

DR WPI; 2001-061214/07.

XX Modulating a biological function of a haematopoietic cell for treating
 PT an allergic response, or diseases mediated by immune system cells,
 PT comprises introducing into the cell a PDZ-PL interaction enhancer or
 PT inhibitor

XX Disclosure: Page 54; 143pp; English.

XX The present invention relates to a method for modulating a biological
 CC function of an endothelial cell or haematopoietic cell, comprises
 CC introducing into a cell an antagonist that inhibits binding between a
 CC PDZ domain protein and a PL domain protein to result in inhibition of
 CC leukocyte activation. The present sequence is a PL peptide. PDZ domains
 CC of proteins are named after three prototypical proteins: PSD95,
 CC Drosophila large disc protein and Zonula Occludin 1 protein. PDZ domain
 CC proteins are involved in synapse formation by organising transmembrane

CC neurotransmitter receptors through intracellular interactions. The
 CC inhibitors identified by the present invention can be used to treat a
 CC disease mediated by haematopoietic cells, e.g. autoimmune disease,
 CC inflammation, allergy (e.g. drug allergies), inflammatory bowel diseases,
 CC ulcerative colitis, ileitis, psoriasis, respiratory allergic diseases
 CC (e.g. asthma), atopic dermatitis, autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, insulin-dependent diabetes, Hashimoto
 CC thyroiditis, osteoarthritis), atherosclerosis, cancers, infectious
 CC diseases (e.g. viral infection), ischaemia, vasculitis and Crohn's
 CC disease. The inhibitors can also be used to prevent transplantation
 CC rejection of a solid organ transplant.

CC Sequence 20 AA:

Query Match 30.0%; Score 15; DB 22; Length 20;
 Best Local Similarity 40.0%; Pred. No. 4.1e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
 1 : 1
 3 PSSSY 7

RESULT 38

AAP93300 ID AAP93300 standard; peptide; 21 AA.

XX AAP93300;

DT 17-DEC-2001 (updated)

DT 11-APR-1990 (first entry)

DE Sequence of Chlamydia trachomatis serovars D major outer membrane protein
 variable domain D-VDII.

XX Chlamydia trachomatis serovars D; variable domain D-VDII;

KW major outer membrane protein; monoclonal antibody; vaccine.

OS Chlamydia trachomatis serovars D.

PN USN7324664-N.

XX 29-AUG-1989.

PE 17-MAR-1989; 89US-0324664.

PR 17-MAR-1989; 89US-0324664.

PA (USSH) US DEPT. OF HEALTH AND HUMAN SERVICES.

PI Caldwell HD, Ying Y, Zhang YX, Watkins NG;

DR WPI: 1989-339697/46.

XX N-PSDB; AAN92136.

PT Chlamydia trachomatis genes - used for determ. of nucleotide and amino
 sequences of the variable domains of the major outer membrane proteins.
 XX Disclosure; Fig. 7; 49pp; English.

CC The major neutralising and serotyping antigenic determinants have been
 CC located in the variable domain. The variable domain is recognised by
 CC MOMP specific monoclonal antibodies. The peptide will be useful in the
 CC construction of chlamydial vaccines. It will also allow prodn. of
 CC reagents and methods for development of new diagnostic tests for
 CC C. trachomatis infections and serological tests for serotyping.

CC (Note: Revised entry submitted to correct the patent number format of
 CC US Government-owned NTIS applications to prevent clashes with ongoing US
 CC granted patent numbers. For further information please visit the Derwent
 CC web site at www.derwent.com/dwpi/updates/ntis_us.html.)

XX Sequence 21 AA:

Query Match 30.0%; Score 15; DB 10; Length 21;
 Best Local Similarity 40.0%; Pred. No. 4.3e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
 1 : 1
 14 PNMSF 18

RESULT 39

AAP93322 ID AAP93322 standard; peptide; 21 AA.

XX AAP93322;

DT 17-DEC-2001 (updated)

DT 12-APR-1990 (first entry)

DE Chlamydia trachomatis serovars LI major outer membrane protein
 variable domain LI-VDII.

XX Chlamydia trachomatis serovars LI; variable domain LI-VDII;

KW major outer membrane protein; monoclonal antibody; vaccine.

OS Chlamydia trachomatis serovars LI.

PN USN7324664-N.

XX 29-AUG-1989.

PE 17-MAR-1989; 89US-0324664.

PR 17-MAR-1989; 89US-0324664.

PA (USSH) US DEPT. OF HEALTH AND HUMAN SERVICES.

PI Caldwell HD, Ying Y, Zhang YX, Watkins NG;

DR WPI: 1989-339697/46.

XX N-PSDB; AAN92144.

PT Chlamydia trachomatis genes - used for determ. of nucleotide and amino
 sequences of the variable domains of the major outer membrane proteins.
 XX Disclosure; Fig. 9; 49pp; English.

CC The major neutralising and serotyping antigenic determinants have been
 CC located in the variable domain. The variable domain is recognised by
 CC MOMP specific monoclonal antibodies. The peptide will be useful in the
 CC construction of chlamydial vaccines. It will also allow prodn. of
 CC reagents and methods for development of new diagnostic tests for
 CC C. trachomatis infections and serological tests for serotyping.

CC (Note: Revised entry submitted to correct the patent number format of
 CC US Government-owned NTIS applications to prevent clashes with ongoing US
 CC granted patent numbers. For further information please visit the Derwent
 CC web site at www.derwent.com/dwpi/updates/ntis_us.html.)

XX Sequence 21 AA:

Query Match 30.0%; Score 15; DB 10; Length 21;
 Best Local Similarity 40.0%; Pred. No. 4.3e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
 1 : 1
 14 PNMSF 18

RESULT 40

AAP98419 ID AAP98419 standard; Protein; 21 AA.

XX AAP98419;

XX 17-DEC-2001 (updated)
 DT 06-MAR-1992 (first entry)
 XX
 DE Sequence of C. trachomatis serovar D major outer membrane protein (MOMP)
 DE variable domain (VD) D-VDII encoded by base pairs 481-543.
 XX
 KW Chlamydia trachomatis; antigen; monoclonal antibody; vaccine;
 KW diagnosis; serotyping; non-immunologic assay.
 XX
 OS Chlamydia trachomatis.
 XX
 PN USN7324664-N.
 XX
 PD 29-AUG-1989.
 XX
 PF 17-MAR-1989; 89US-0324664.
 XX
 PR 17-MAR-1989; 89US-0324664.
 XX
 PA (USSH). US DEPT HEALTH & HUMAN.
 XX
 PI Caldwell HD, Ying Y, Zhang YX, Watkins NG;
 XX
 DR WPI: 1989-339697/46.
 DR N-PSDB; AAN97054.
 XX
 PT Chlamydia trachomatis genes - used for determ. of nucleotide and
 PT amino sequences of the variable domains of the major outer
 XX
 PS membrane proteins
 XX
 PS disclosure; Fig 7; 49pp; English.
 XX
 CC The inventors sequenced the 4 MOMP VDs of ten C. trachomatis
 CC serovars and the amino acid sequences were deduced. The MOMP VDs
 CC with the greatest total hydrophilicity and charge values were found
 CC to be the location of antigenic determinants recognised by MOMP
 CC specific monoclonal antibodies. The nucleotide, amino acid
 CC sequences and hydrophilicity/charge value analyses will assist in
 CC the selection of appropriate MOMP antigenic determinants to be used
 CC in the construction of synthetic peptides, subunits or recombinant
 CC chlamydial vaccines. This will allow the prodn. or reagents and
 CC methodologies applicable in the development of new diagnostic tests
 CC for serotyping.
 CC (Note: Revised entry submitted to correct the patent number format of
 CC US Government-owned NTIS applications to prevent clashes with ongoing US
 CC granted patent numbers. For further information please visit the Derwent
 CC web site at www.derwent.com/dwpi/updates/ntis_us.html.)
 XX
 SQ Sequence 21 AA;
 Query Match 30.0%; Score 15; DB 10; Length 21;
 Best Local Similarity 40.0%; Pred. No. 4.3e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 PXXXX 5
 II :
 DB 14 PNMSP 18
 XX
 RESULT 41
 AAP98427
 ID AAP98427 standard; Protein: 21 AA.
 XX
 AC AAP98427;
 XX
 DT 17-DEC-2001 (updated)
 DT 06-MAR-1992 (first entry)
 XX
 DE Sequence of C. trachomatis serovar L1 major outer membrane protein (MOMP)
 DE variable domain (VD) L1-VDII encoded by base pairs 481-543.
 XX
 KW Chlamydia trachomatis; antigen; monoclonal antibody; vaccine;

KW diagnosis; serotyping; non-immunologic assay.
 XX
 OS Chlamydia trachomatis.
 XX
 PN USN7324664-N.
 XX
 PD 29-AUG-1989.
 XX
 PF 17-MAR-1989; 89US-0324664.
 XX
 PR 17-MAR-1989; 89US-0324664.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN.
 XX
 PI Caldwell HD, Ying Y, Zhang YX, Watkins NG;
 XX
 DR WPI: 1989-339697/46.
 DR N-PSDB; AAN97052.
 XX
 PT Chlamydia trachomatis genes - used for determ. of nucleotide and
 PT amino sequences of the variable domains of the major outer
 XX
 PS membrane proteins
 XX
 PS disclosure; Fig 9; 49pp; English.
 XX
 CC The inventors sequenced the 4 MOMP VDs of ten C. trachomatis
 CC serovars and the amino acid sequences were deduced. The MOMP VDs
 CC with the greatest total hydrophilicity and charge values were found
 CC to be the location of antigenic determinants recognised by MOMP
 CC specific monoclonal antibodies. The nucleotide, amino acid
 CC sequences and hydrophilicity/charge value analyses will assist in
 CC the selection of appropriate MOMP antigenic determinants to be used
 CC in the construction of synthetic peptides, subunits or recombinant
 CC chlamydial vaccines. This will allow the prodn. or reagents and
 CC methodologies applicable in the development of new diagnostic tests
 CC for serotyping.
 CC (Note: Revised entry submitted to correct the patent number format of
 CC US Government-owned NTIS applications to prevent clashes with ongoing US
 CC granted patent numbers. For further information please visit the Derwent
 CC web site at www.derwent.com/dwpi/updates/ntis_us.html.)
 XX
 SQ Sequence 21 AA;
 Query Match 30.0%; Score 15; DB 10; Length 21;
 Best Local Similarity 40.0%; Pred. No. 4.3e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 PXXXX 5
 II :
 DB 14 PNMSP 18
 XX
 RESULT 42
 AAM46505
 ID AAM46505 standard; Peptide: 21 AA.
 XX
 AC AAM46505;
 XX
 DT 18-MAY-1998 (first entry)
 XX
 DE Peptide 5 of the alpha-glucuronidase protein.
 XX
 KW Alpha-glucuronidase; Aspergillus tubigenis NW756; overexpression; treat;
 KW cellulosic pulp; removal; glucuronic acid; silaging additive;
 KW degradation; plant matter; animal feed; metal ion; bioavailability.
 XX
 OS Aspergillus tubigenis.
 XX
 PN WO9743423-A2.
 XX
 PD 20-NOV-1997.
 XX
 PF 12-MAY-1997; 97WO-DK00218.

```

XX 10-MAY-1996; 96DK-0000565.
PR (DANI-) DANISCO AS.
XX
XX De Vries RP, Poulsen CH, Visser J, Zargahi MR;
XX WPI; 1998-008892/01.
DR N-PSDB; AAV05187.
XX
XX DNA encoding alpha-glucuronidase from Aspergillus, related vectors
XX PT and transformants used as bread improvers, for increasing
XX PT digestibility of animal feeds and in processing of cellulosic pulp
XX PS
XX Claim 2; Page 66; 90pp; English.
XX
XX Peptides AAW46500-511 are peptides derived from the alpha-glucuronidase
XX CC protein of Aspergillus tubigenis NW756. The peptides were used to
XX CC design PCR primers which were used to amplify an A. tubigenis genomic
XX CC library. The 1142 bp amplicon was used to screen the same library to
XX CC isolate the full length sequence of the alpha-glucuronidase gene
XX CC (AAV05187). The alpha-glucuronidase gene, including the flanking regions,
XX CC was cloned as a 6.5 kb XhoI-BamHI fragment, for overexpression of the
XX CC protein. Cells transformed with vectors containing the
XX CC alpha-glucuronidase gene are cultured to produce the protein. The
XX CC alpha-glucuronidase protein is used to improve dough and baked products.
XX CC The protein can also be used to treat cellulosic pulp to remove at least
XX CC some of the glucuronic acid residues present in it, as a silaging
XX CC additive and to degrade plant matter generally. When added to animal feed
XX CC (particularly waste products of annual plants such as beet pulp, cereal
XX CC bran or straw) the protein increases feed utilisation and feed conversion
XX CC rate, particularly by increasing bioavailability of metal ions.
XX
XX Sequence 21 AA;
SQ
Query Match 30.0%; Score 15; DB 19; Length 21;
Best Local Similarity 27.3%; Pred. NO. 4.3e+03;
Matches 3; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
QY 1 PNXVXXXXXX 11
   | : |
Db 2 PSGVYDGVNY 12

```

RESULT 43
AAV05690
ID AAV05690 standard; Peptide; 21 AA.
XX
AC AAV05690;
XX
DT 19-JUL-1999 (first entry)
XX
DE Human tumour necrosis factor receptor ZTNFR-6 antigenic peptide.
XX
KW ZTNFR-6; tumour necrosis factor receptor-6; human;
XX cell maturation; bone cell regulation; antigen; antibody.
XX
OS Homo sapiens.
XX
PN WO9911790-A1.
XX
PD 11-MAR-1999.
XX
XX 03-SEP-1998; 98WO-US18364.
XX
XX 04-SEP-1997; 97US-0923725.
PR 04-SEP-1997; 97US-0057608.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Farrah TM, Gross JA, Matthews SM;
XX WPI; 1999-205190/17.
DR

```

XX New secreted or membrane bound tumor necrosis factor receptor
XX PT ZTNFR-6 - useful for detecting a genetic abnormality in a patient
XX
XX Example 8; Page 142; 145pp; English.
XX
XX This antigenic peptide corresponds to amino acid residues 205-224
XX CC of ZTNFR-6 (see AAV05678), a novel human tumour necrosis factor
XX CC receptor. It was used to raise polyclonal anti-peptide
XX CC antibody, designated RbAlphazTNFR-2, in New Zealand white
XX CC rabbits. Antibodies raised against ZTNFR-6 are useful for
XX CC immunohistochemical tagging of cells expressing ZTNFR-6 for use
XX CC in diagnosis, isolating ZTNFR-6, generating anti-idiotypic
XX CC antibodies, and as neutralising antibodies or antagonists that
XX CC block ZTNFR-6 in vivo and in vitro.
XX
XX Sequence 21 AA;
SQ
Query Match 30.0%; Score 15; DB 20; Length 21;
Best Local Similarity 40.0%; Pred. NO. 4.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 PNXV 5
   | : |
Db 14 PSSRY 18

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RESULT 44
AAW73979
ID AAW73979 standard; peptide; 21 AA.
XX
AC AAW73979;
XX
DT 04-MAY-1999 (first entry)
XX
DE C. trachomatis serovar D, MOMP variable domain sequence #2.
XX
XX
KW Variable domain; MOMP; major outer membrane protein; subunit vaccine;
XX C. trachomatis infection; serotyping; diagnosis.
XX
OS Chlamydia trachomatis.
XX
PN US5869608-A.
XX
PD 09-FEB-1999.
XX
PF 16-MAR-1992; 92US-0853359.
XX
XX 17-MAR-1989; 89US-0324664.
PR 16-MAR-1992; 92US-0853359.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Caldwell HD, Watkins NG, Ying Y, Zhang Y;
XX WPI; 1999-152876/13.
XX
XX Chlamydia trachomatis peptides - and DNA fragments encoding them
XX PS
XX Claim 2; Column 13; 29pp; English.
XX
XX This sequence represents a variable domain of the major outer membrane
XX CC protein (MOMP) of Chlamydia trachomatis serovar D. The invention relates
XX CC to variable domain fragments of the MOMP of Chlamydia trachomatis
XX CC serovar Ba, serovar D, serovar E, serovar F, serovar G, serovar H,
XX CC serovar I, serovar J, serovar K, and serovar L3, and to DNA sequences
XX CC encoding them. The peptides are useful in diagnostic tests for
XX CC C. trachomatis infections, serological tests for serotyping, and as
XX CC subunit vaccines.
XX
XX Sequence 21 AA;
SQ

Query Match 30.0%; Score 15; DB 20; Length 21;

Best Local Similarity 40.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
11
DB 14 PNMSF 18

RESULT 45

AAB23881
ID AAB23881 standard; peptide; 21 AA.

AC AAB23881;

DT 17-JAN-2001 (first entry)

DE Artificial sequence designed peptide #6.

KW Peptide synthesis; chemical synthesis; solid phase synthesis.

OS Synthetic;

PN WO200055182-A1.

PD 21-SEP-2000.

PF 15-MAR-2000; 2000WO-JP01584.

PR 15-MAR-1999; 99JP-0067917.

PA (SANY) SANKYO CO LTD.

PI Kawaguchi J, Serizawa N;

DR WPI; 2000-602106/57.

PT Chemically synthesizing a peptide by solid phase synthesis by adding
PT protective group to inactivate part of alpha amino group of an amino
PT acid group

PS Example 2; Page 13; 38pp; Japanese.

CC The present invention describes a method for chemically synthesizing a
CC peptide by solid phase synthesis. The method comprises processing a
CC carrier resin to which the C-terminal amino acid derivative of the
CC target peptide has been preliminarily bonded is characterised by adding
CC a protective group to inactivate a part of alpha-amino groups of an
CC amino acid capable of undergoing a peptide extension reaction on the
CC carrier resin. The method is useful for synthesising a peptide by solid
CC phase synthesis. Long chain peptides can be readily synthesised in with
CC a high success ratio without using the segment condensation method or
CC gene manipulations. The present sequence represents an amino acid
CC peptide sequence given in an example from the present invention.

SO Sequence 21 AA;

Query Match 30.0%; Score 15; DB 21; Length 21;
Best Local Similarity 27.3%; Pred. No. 4.3e+03;

Matches 3; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 PNXXYXXXXXX 11
11
DB 2 PSGKYEKGNIY 12

RESULT 46

AAB23892
ID AAB23892 standard; peptide; 21 AA.

AC AAB23892;

DT 17-JAN-2001 (first entry)

DE Artificial sequence designed peptide #15.

KW Peptide synthesis; chemical synthesis; solid phase synthesis.

OS Synthetic.

PN WO200055182-A1.

PD 21-SEP-2000.

PF 15-MAR-2000; 2000WO-JP01584.

PR 15-MAR-1999; 99JP-0067917.

PA (SANY) SANKYO CO LTD.

PI Kawaguchi J, Serizawa N;

DR WPI; 2000-602106/57.

PT Chemically synthesizing a peptide by solid phase synthesis by adding
PT protective group to inactivate part of alpha amino group of an amino
PT acid group

PS Example 4; Page 18; 38pp; Japanese.

CC The present invention describes a method for chemically synthesizing a
CC peptide by solid phase synthesis. The method comprises processing a
CC carrier resin to which the C-terminal amino acid derivative of the
CC target peptide has been preliminarily bonded is characterised by adding
CC a protective group to inactivate a part of alpha-amino groups of an
CC amino acid capable of undergoing a peptide extension reaction on the
CC carrier resin. The method is useful for synthesising a peptide by solid
CC phase synthesis. Long chain peptides can be readily synthesised in with
CC a high success ratio without using the segment condensation method or
CC gene manipulations. The present sequence represents an amino acid
CC peptide sequence given in an example from the present invention.

SO Sequence 21 AA;

Query Match 30.0%; Score 15; DB 21; Length 21;
Best Local Similarity 27.3%; Pred. No. 4.3e+03;

Matches 3; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 PNXXYXXXXXX 11
11
DB 2 PSGKYEKGNIY 12

RESULT 47

AAB23903
ID AAB23903 standard; peptide; 21 AA.

AC AAB23903;

DT 17-JAN-2001 (first entry)

DE Artificial sequence designed peptide #24.

KW Peptide synthesis; chemical synthesis; solid phase synthesis.

OS Synthetic.

PN WO200055182-A1.

PD 21-SEP-2000.

PF 15-MAR-2000; 2000WO-JP01584.

PR 15-MAR-1999; 99JP-0067917.

PA (SANY) SANKYO CO LTD.

SQ Sequence 21 AA;

Query Match 30.0%; Score 15; DB 23; Length 21;
 Best Local Similarity 40.0%; Pred. No. 4.3e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
 11 :
 Db 14 PNMSF 18

RESULT 50

ABG68826

ID ABG68826 standard; Peptide: 21 AA.

XX AC ABG68826;

DT 07-OCT-2002 (first entry)

DE Chlamydia trachomatis MOMP variable domain (VD) associated peptide #2.

KW Major outer membrane protein; MOMP; variable domain; VD; serotyping;
 KM Species identification; antibacterial; vaccine; serovar D.

XX OS Chlamydia trachomatis.

PN US6384206-B1.

PD 07-MAY-2002.

PF 09-FEB-1999; 99US-0247137.

PR 17-MAR-1989; 89US-0324664.

PR 16-MAR-1992; 92US-0853359.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Caldwell HD, Ying Y, Zhang Y, Watkins NG;

XX DR WPI; 2002-451393/48.

XX DR N-PSDB; ABK97793.

XX PT New nucleic acid encoding variable regions of Chlamydia trachomatis
 PT outer membrane protein, useful e.g. for serotyping and vaccine
 development

XX PS Claim 1 : Column 13; 28pp; English.

XX CC The present invention relates to a new nucleic acid encoding polypeptides
 CC comprising any of four amino acid sequences representing the four
 CC variable domains in the major outer membrane protein of serovar D of
 CC C. trachomatis. These proteins are useful in arrays of oligopeptides for
 CC species identification or serotyping of C. trachomatis. The molecules of
 CC the invention are also useful in selection of antigenic determinants for
 CC use in synthetic peptides, subunits and recombinant anti-Chlamydia
 CC vaccines. The present amino acid sequence represents a Chlamydia
 CC trachomatis major outer membrane protein (MOMP) variable domain (VD)
 CC associated peptide of the invention, as described above.

XX SQ Sequence 21 AA;

Query Match 30.0%; Score 15; DB 23; Length 21;
 Best Local Similarity 40.0%; Pred. No. 4.3e+03;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
 11 :
 Db 14 PNMSF 18

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OM protein - protein search, using sw model

Run on: June 11, 2003, 07:44:04 ; Search time 245 Seconds

(without alignments)
8.849 Million cell updates/sec

Title: US-09-883-727A-127

Perfect score: 50

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Gapop 10.0 , Gapext 0.5

Searched: 392085 segs, 103240269 residues

Total number of hits satisfying chosen parameters: 4649

Minimum DB seq length: 20

Maximum DB seq length: 21

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 150 summaries

Database :

Published Applications AA: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	17	34.0	20	9	US-09-880-748-2819
5	17	34.0	20	9	US-09-880-748-2843
6	16	32.0	21	9	US-09-880-748-2769
7	16	32.0	21	10	US-09-883-727A-126
8	16	32.0	21	10	US-09-883-727A-125
9	15	30.0	20	9	US-09-883-727A-128
10	15	30.0	20	9	US-09-973-025-86
11	15	30.0	20	9	US-09-899-303-86
12	15	30.0	20	9	US-09-750-754-50
13	14	28.0	20	9	US-09-995-808-86
14	14	28.0	20	1	US-08-677-599B-6
15	14	28.0	20	1	US-08-677-599B-7
16	14	28.0	20	9	US-10-097-065-636
17	14	28.0	20	9	US-09-880-748-3053
18	14	28.0	21	9	US-09-881-572A-10
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			21	9	US-09-880-748-2763

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22	14	28.0	21	9	US-10-150-111-174	Sequence 174, App
23	14	28.0	21	10	US-09-879-228-9	Sequence 9, Appli
24	14	28.0	21	10	US-09-864-761-40485	Sequence 40485, A
25	13	26.0	20	8	US-08-424-550B-341	Sequence 341, App
26	13	26.0	20	9	US-10-007-270-19	Sequence 29, Appl
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35	13	26.0	20	9	US-09-795-211-3	Sequence 3, Appli
36	13	26.0	20	9	US-09-973-025-57	Sequence 57, Appl
37	13	26.0	20	9	US-09-973-025-58	Sequence 58, Appl
38	13	26.0	20	9	US-10-012-896-495	Sequence 495, App
39	13	26.0	20	9	US-09-895-793-495	Sequence 495, App
40	13	26.0	20	9	US-09-849-626-1843	Sequence 495, App
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54	13	26.0	20	9	US-10-097-175-80	Sequence 80, Appl
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56	13	26.0	20	9	US-10-062-710-95	Sequence 95, Appl
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58	13	26.0	20	9	US-09-931-325A-4	Sequence 4, Appli
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91	13	26.0	20	10	US-09-839-447A-32	Sequence 32, Appl
92	13	26.0	20	10	US-09-839-447A-107	Sequence 107, App

93	13	26.0	20	10	US-09-839-447A-108	Sequence 108, App
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95	13	26.0	20	10	US-09-825-882-31	Sequence 31, Appl
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113	13	26.0	21	9	US-09-895-793-521	Sequence 521, App
114	13	26.0	21	9	US-09-895-814-496	Sequence 496, App
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117	13	26.0	21	9	US-09-880-505-6	Sequence 6, Appl
118	13	26.0	21	9	US-09-387-340-43	Sequence 43, Appl
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120	13	26.0	21	9	US-09-974-879-539	Sequence 539, App
121	13	26.0	21	9	US-09-809-391-324	Sequence 324, App
122	13	26.0	21	9	US-10-053-485-64	Sequence 64, Appl
123	13	26.0	21	9	US-10-062-710-30	Sequence 30, Appl
124	13	26.0	21	9	US-10-062-710-63	Sequence 63, Appl
125	13	26.0	21	9	US-10-062-710-157	Sequence 157, Appl
126	13	26.0	21	9	US-09-931-325A-61	Sequence 61, Appl
127	13	26.0	21	9	US-09-931-325A-73	Sequence 73, Appl
128	13	26.0	21	9	US-10-046-801-13	Sequence 13, Appl
129	13	26.0	21	9	US-10-097-065-542	Sequence 542, App
130	13	26.0	21	9	US-09-880-748-2172	Sequence 2172, App
131	13	26.0	21	9	US-09-880-748-3021	Sequence 3021, App
132	13	26.0	21	9	US-09-880-748-3068	Sequence 3068, App
133	13	26.0	21	9	US-09-880-748-3072	Sequence 3072, App
134	13	26.0	21	9	US-09-880-748-3163	Sequence 3163, App
135	13	26.0	21	9	US-09-880-748-3219	Sequence 3219, App
136	13	26.0	21	9	US-10-145-415-62	Sequence 62, Appl
137	13	26.0	21	9	US-10-057-789-159	Sequence 159, App
138	13	26.0	21	9	US-10-057-789-280	Sequence 280, App
139	13	26.0	21	9	US-10-245-616-4	Sequence 4, Appl
140	13	26.0	21	9	US-09-305-736-290	Sequence 290, App
141	13	26.0	21	9	US-09-305-736-541	Sequence 541, App
142	13	26.0	21	9	US-10-010-940-496	Sequence 496, App
143	13	26.0	21	9	US-10-010-940-521	Sequence 521, App
144	13	26.0	21	9	US-10-212-628-159	Sequence 159, App
145	13	26.0	21	9	US-10-212-628-280	Sequence 280, App
146	13	26.0	21	9	US-09-386-591-43	Sequence 43, Appl
147	13	26.0	21	9	US-10-008-277B-3	Sequence 3, Appl
148	13	26.0	21	10	US-09-739-907-112	Sequence 112, App
149	13	26.0	21	10	US-09-729-835-85	Sequence 85, Appl
150	13	26.0	21	10	US-09-799-463-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-883-727A-129
; Sequence 129, Application US/09883727A
; Patent No. US20020102256A1
; GENERAL INFORMATION:
; APPLICANT: West, Robert R.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Fox, Brian
; TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of
; Complement C1s

FILE REFERENCE: 00-33
CURRENT APPLICATION NUMBER: US/09/883,727A
CURRENT FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 129
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Formula of a complement C1s inhibitor
NAME/KEY: VARIANT
LOCATION: (3)...(3)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: VARIANT
LOCATION: (4)...(4)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: MUTAGEN
LOCATION: (6)...(6)
OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
NAME/KEY: MUTAGEN
LOCATION: (7)...(7)
OTHER INFORMATION: Xaa = sulfated tyrosine
NAME/KEY: MUTAGEN
LOCATION: (8)...(8)
OTHER INFORMATION: Xaa = 2-sulfotyrosine
NAME/KEY: VARIANT
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: VARIANT
LOCATION: (10)...(10)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: MUTAGEN
LOCATION: (12)...(12)
OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
NAME/KEY: MUTAGEN
LOCATION: (13)...(13)
OTHER INFORMATION: Xaa = sulfated tyrosine
NAME/KEY: MUTAGEN
LOCATION: (14)...(14)
OTHER INFORMATION: Xaa = 2-sulfotyrosine
NAME/KEY: VARIANT
LOCATION: (15)...(15)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: MUTAGEN
LOCATION: (17)...(17)
OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
NAME/KEY: MUTAGEN
LOCATION: (18)...(18)
OTHER INFORMATION: Xaa = sulfated tyrosine
NAME/KEY: MUTAGEN
LOCATION: (19)...(19)
OTHER INFORMATION: Xaa = 2-sulfotyrosine
NAME/KEY: VARIANT
LOCATION: (20)...(20)
OTHER INFORMATION: Xaa = D or E
US-09-883-727A-129

Query Match 46.0%; Score 23; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PNXXXXXXXXXXX 16
DB 1 PNXXXXXXXXXXX 16

RESULT 2
US-09-883-727A-127
; Sequence 127, Application US/09883727A
; Patent No. US20020102256A1
; GENERAL INFORMATION:
; APPLICANT: West, Robert R.

```
APPLICANT: Shepard, Paul O.
TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of
FILE REFERENCE: 00-33
CURRENT APPLICATION NUMBER: US/09/883,727A
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 127
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: VARIANT
LOCATION: (3)...(3)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: VARIANT
LOCATION: (4)...(4)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: MUTAGEN
LOCATION: (6)...(6)
OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
NAME/KEY: MUTAGEN
LOCATION: (7)...(7)
OTHER INFORMATION: Xaa = sulfated tyrosine
NAME/KEY: MUTAGEN
LOCATION: (8)...(8)
OTHER INFORMATION: Xaa = 2-sulfotyrosine
NAME/KEY: VARIANT
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: VARIANT
LOCATION: (10)...(10)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: MUTAGEN
LOCATION: (12)...(12)
OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
NAME/KEY: MUTAGEN
LOCATION: (13)...(13)
OTHER INFORMATION: Xaa = sulfated tyrosine
NAME/KEY: MUTAGEN
LOCATION: (14)...(14)
OTHER INFORMATION: Xaa = 2-sulfotyrosine
NAME/KEY: VARIANT
LOCATION: (15)...(15)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: MUTAGEN
LOCATION: (17)...(17)
OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
NAME/KEY: MUTAGEN
LOCATION: (18)...(18)
OTHER INFORMATION: Xaa = sulfated tyrosine
NAME/KEY: MUTAGEN
LOCATION: (19)...(19)
OTHER INFORMATION: Xaa = 2-sulfotyrosine
NAME/KEY: VARIANT
LOCATION: (20)...(20)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: VARIANT
LOCATION: (21)...(21)
OTHER INFORMATION: Xaa = D or E, or is absent
US-09-883-727a-127

Query Match
Best Local Similarity 100.0%; Score 23; DB 10; Length 21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 3
US-10-032-482-23
Sequence 23, Application US/10032482
Publication No. US20020197270A1
GENERAL INFORMATION:
APPLICANT: Cohen, Itun
APPLICANT: ROTHER, Varda
APPLICANT: Wolkowicz, Roland
APPLICANT: Ruiz, Pedro
APPLICANT: BEREZ-ALON, Neta
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR
FILE REFERENCE: COHEN42
CURRENT APPLICATION NUMBER: US/10/032,482
CURRENT FILING DATE: 2002-01-02
PRIOR APPLICATION NUMBER: US/09/445,602
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: PCT/IL98/00266
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: IL 121041
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 20
TYPE: PRT
ORGANISM: Mus musculus
US-10-032-482-23
```

```
Query Match
Best Local Similarity 60.0%; Score 18; DB 9; Length 20;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 PNXXY 5
DB 5 PNNXY 9
```

```
RESULT 4
US-09-880-748-2819
Sequence 2819, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2819
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-2819
```

```
Query Match
Best Local Similarity 34.0%; Score 17; DB 9; Length 20;
Matches 4; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
```

```
QY 2 NXXYXXXXXXYY 16
```

Db 2 NADYDILGTGYPRDY 16

RESULT 5

US-09-880-748-2843
; Sequence 2843, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PE523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2843
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2843

Query Match

Best Local Similarity 34.0%; Score 17; DB 9; Length 20;
Matches 4; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 PNXXYXXXXXXYY 16
; 1: - - - - -
Db 2 PSPYDILGTGYLPY 17

RESULT 6

US-09-880-748-2769
; Sequence 2769, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PE523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2769
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2769

Query Match 32.0%; Score 16; DB 9; Length 21;
Best Local Similarity 26.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2 NXYYXXXXXXYY 16
; 1: - - - - -
Db 1 NGYDILGTGYLMDY 15

RESULT 7

US-09-883-727a-126
; Sequence 126, Application US/09883727a
; Patent No. US20020102256A1
; GENERAL INFORMATION:
; APPLICANT: West, Robert R.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Fox, Brian
; TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of
; FILE REFERENCE: 00-33
; CURRENT APPLICATION NUMBER: US/09/883,727a
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 126
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa = A or P
; NAME/KEY: VARIANT
; LOCATION: (3)...(3)
; OTHER INFORMATION: Xaa = D or E
; NAME/KEY: VARIANT
; LOCATION: (4)...(4)
; OTHER INFORMATION: Xaa = D or E
; NAME/KEY: MUTAGEN
; LOCATION: (6)...(6)
; OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
; NAME/KEY: MUTAGEN
; LOCATION: (7)...(7)
; OTHER INFORMATION: Xaa = sulfated tyrosine
; NAME/KEY: MUTAGEN
; LOCATION: (8)...(8)
; OTHER INFORMATION: Xaa = 2-sulfotyrosine
; NAME/KEY: VARIANT
; LOCATION: (9)...(9)
; OTHER INFORMATION: Xaa = D or E
; NAME/KEY: VARIANT
; LOCATION: (10)...(10)
; OTHER INFORMATION: Xaa = D or E
; NAME/KEY: MUTAGEN
; LOCATION: (12)...(12)
; OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
; NAME/KEY: MUTAGEN
; LOCATION: (13)...(13)
; OTHER INFORMATION: Xaa = sulfated tyrosine
; NAME/KEY: MUTAGEN
; LOCATION: (14)...(14)
; OTHER INFORMATION: Xaa = 2-sulfotyrosine
; NAME/KEY: VARIANT
; LOCATION: (15)...(15)
; OTHER INFORMATION: Xaa = D or E
; NAME/KEY: MUTAGEN
; LOCATION: (17)...(17)
; OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
; NAME/KEY: MUTAGEN
; LOCATION: (18)...(18)
; OTHER INFORMATION: Xaa = sulfated tyrosine
; NAME/KEY: MUTAGEN
; LOCATION: (19)...(19)
; OTHER INFORMATION: Xaa = 2-sulfotyrosine
; NAME/KEY: VARIANT
; LOCATION: (20)...(20)

OTHER INFORMATION: Xaa = D or E
NAME/KEY: VARIANT
LOCATION: (21)...(21)
OTHER INFORMATION: Xaa = D or E, or is absent
US-09-883-727A-126

Query Match 32.0%; Score 16; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NXXXXXXXXXXXXX 16
Db 2 NXXXXXXXXXXXXX 16

RESULT 8
US-09-883-727A-128
Sequence 128, Application US/09883727A
Patent No. US20020102256A1
GENERAL INFORMATION:
APPLICANT: West, Robert R.
APPLICANT: Sheppard, Paul O.
APPLICANT: Fox, Brian
TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of
FILE REFERENCE: 00-33
CURRENT APPLICATION NUMBER: US/09/883,727A
CURRENT FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 128
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Formula of a C1s exosite binding moiety
NAME/KEY: VARIANT
LOCATION: (3)...(3)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: VARIANT
LOCATION: (4)...(4)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: MUTAGEN
LOCATION: (6)...(6)
OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
NAME/KEY: MUTAGEN
LOCATION: (7)...(7)
OTHER INFORMATION: Xaa = sulfated tyrosine
NAME/KEY: MUTAGEN
LOCATION: (8)...(8)
OTHER INFORMATION: Xaa = 2-sulfotyrosine
NAME/KEY: VARIANT
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: VARIANT
LOCATION: (10)...(10)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: MUTAGEN
LOCATION: (12)...(12)
OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
NAME/KEY: MUTAGEN
LOCATION: (13)...(13)
OTHER INFORMATION: Xaa = sulfated tyrosine
NAME/KEY: MUTAGEN
LOCATION: (14)...(14)
OTHER INFORMATION: Xaa = 2-sulfotyrosine
NAME/KEY: VARIANT
LOCATION: (15)...(15)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: MUTAGEN
LOCATION: (17)...(17)
OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
NAME/KEY: MUTAGEN

LOCATION: (18)...(18)
OTHER INFORMATION: Xaa = sulfated tyrosine
NAME/KEY: MUTAGEN
LOCATION: (19)...(19)
OTHER INFORMATION: Xaa = 2-sulfotyrosine
NAME/KEY: VARIANT
LOCATION: (20)...(20)
OTHER INFORMATION: Xaa = D or E
NAME/KEY: VARIANT
LOCATION: (21)...(21)
OTHER INFORMATION: Xaa = D or E, or is absent
US-09-883-727A-128

Query Match 32.0%; Score 16; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NXXXXXXXXXXXXX 16
Db 2 NXXXXXXXXXXXXX 16

RESULT 9
US-09-973-025-86
Sequence 86, Application US/09973025
Publication No. US20020182706A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
BOSMAN, FONS
DE MARTYNOFF, GUY
BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/973,025
FILING DATE: 10-Oct-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-09-973-025-86

Query Match 30.0%; Score 15; DB 9; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
1: 1
DB 8 PDATY 12

RESULT 10

US-09-899-303-86
Sequence 86, Application US/09899303
Publication No. US20030036110A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
BOSMAN, FONS
DE MARTYNOFF, GUY
BUYSE, MARIE-ANGE

TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,303
FILING DATE: 06-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4000

INFORMATION FOR SEQ ID NO: 86:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:

US-09-899-303-86

Query Match 30.0%; Score 15; DB 9; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
1: 1
DB 8 PDATY 12

RESULT 11

US-09-750-754-50
Sequence 50, Application US/09750754
Publication No. US20030055213A1
GENERAL INFORMATION:

APPLICANT: TANAKA, Takeo
APPLICANT: MORISHITA, Yoshihazu
APPLICANT: MAKINO, Mika
APPLICANT: CHIBA, Shigeru
APPLICANT: KAWAMOTO, Isao

APPLICANT: TSUKUDA, Elji
APPLICANT: YOSHIDA, Mayumi
APPLICANT: BANDO, Chieko
APPLICANT: YAMAGUCHI, Kazuo
APPLICANT: MATSUDA, Yuzuru
TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
STREET: 1300 No. US20030055213A1th Seventeenth Street, Suite 1800
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22209

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/750,754
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/321,625
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: TERRY, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 506.32366PX1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal

US-09-750-754-50

Query Match 30.0%; Score 15; DB 9; Length 20;
Best Local Similarity 27.3%; Pred. No. 1.9e+03;
Matches 3; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 PNXYYXXXXXY 11
1: 1
DB 8 PDWVYFAFFNY 18

RESULT 12

US-09-995-808-86
Sequence 86, Application US/09995808
Publication No. US20030095980A1
GENERAL INFORMATION:

APPLICANT: Inogenetics N.V.
TITLE OF INVENTION: Purified hepatitis C virus envelope proteins for diagnostic an
FILE REFERENCE: 2551-70
CURRENT APPLICATION NUMBER: US/09/995,808
CURRENT FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin 3.1
SEQ ID NO: 86

LENGTH: 20
TYPE: PRT
ORGANISM: Hepatitis C virus

US-09-995-808-86

Query Match 30.0%; Score 15; DB 9; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
1: |
Db 8 PDAEY 12

RESULT 13
US-08-677-599B-6
; Sequence 6, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,599B
; FILING DATE: 08-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50161-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212/278/0400
; TELEFAX: 212/391/0525
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-677-599B-6

Query Match 28.0%; Score 14; DB 1; Length 20;
Best Local Similarity 40.0%; Pred. No. 3.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
1: |
Db 14 PDAEY 18

RESULT 14
US-08-677-599B-7
; Sequence 7, Application US/08677599B
; Patent No. US20020155117A1
; GENERAL INFORMATION:
; APPLICANT: Sucia-Foca, Nicole
; TITLE OF INVENTION: METHODS FOR DETECTING ORGAN ALLOGRAFT
; TITLE OF INVENTION: REJECTION AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York

COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,599B
FILING DATE: 08-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 50161-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212/278/0400
TELEFAX: 212/391/0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-599B-7

Query Match 28.0%; Score 14; DB 1; Length 20;
Best Local Similarity 40.0%; Pred. No. 3.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
1: |
Db 6 PDAEY 10

RESULT 15
US-10-097-065-636
; Sequence 636, Application US/10097065
; Publication No. US20030055236A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: P2021P1
; CURRENT APPLICATION NUMBER: US/10/097,065
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,008
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,365

;; PRIOR FILING DATE: 1997-12-19
;; NUMBER OF SEQ ID NOS: 672
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 636
;; LENGTH: 20
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-097-065-636

Query Match 28.0%; Score 14; DB 9; Length 20;
Best Local Similarity 40.0%; Pred. No. 3.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
1: 1
DB 2 PSRRY 6

RESULT 16
US-09-880-748-3053
;; Sequence 3053, Application US/09880748
;; Publication No. US2003005937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 3053
;; LENGTH: 20
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-3053

Query Match 28.0%; Score 14; DB 9; Length 20;
Best Local Similarity 40.0%; Pred. No. 3.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
1: 1
DB 12 PSRRY 16

RESULT 17
US-09-881-572A-10
;; Sequence 10, Application US/09881572A
;; Patent No. US20020164583A1
;; GENERAL INFORMATION:
;; APPLICANT: Roth, Monica;
;; APPLICANT: Bupp, Keith;
;; APPLICANT: University of Medicine and Dentistry of New Jersey
;; TITLE OF INVENTION: Targeting Viral Vectors to Specific Cells
;; FILE REFERENCE: 601-1-095
;; CURRENT APPLICATION NUMBER: US/09/881,572A
;; CURRENT FILING DATE: 2002-03-05
;; PRIOR APPLICATION NUMBER: 60/212,239
;; PRIOR FILING DATE: 2000-06-16
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: Patentln version 3.0
;; SEQ ID NO 10
;; LENGTH: 21
;; TYPE: PRT
;; ORGANISM: Homo sapiens

;; TYPE: PRT
;; ORGANISM: Rat Leukemia Virus
US-09-881-572A-10

Query Match 28.0%; Score 14; DB 9; Length 21;
Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
1: 1
DB 10 PHSY 14

RESULT 18
US-09-942-185-5
;; Sequence 5, Application US/09942185
;; Patent No. US20020165113A1
;; GENERAL INFORMATION:
;; APPLICANT: Aehle, Wolfgang
;; APPLICANT: Covents, Daniel
;; APPLICANT: Doornink, Monique
;; APPLICANT: van Gastel, Frans
;; APPLICANT: Rodrigues, Ana
;; APPLICANT: Topozada, Amr
;; APPLICANT: De Vries, Cornelis Hendrikus
;; TITLE OF INVENTION: Detergent Compositions Comprising No. US20020165113A1el Phenol
;; FILE REFERENCE: C7567
;; CURRENT APPLICATION NUMBER: US/09/942,185
;; CURRENT FILING DATE: 2001-08-29
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 5
;; LENGTH: 21
;; TYPE: PRT
;; ORGANISM: Stachybotrys chartarum
US-09-942-185-5

Query Match 28.0%; Score 14; DB 9; Length 21;
Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
1: 1
DB 10 PHSY 14

RESULT 19
US-09-880-748-2763
;; Sequence 2763, Application US/09880748
;; Publication No. US2003005937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 2763
;; LENGTH: 21
;; TYPE: PRT
;; ORGANISM: Homo sapiens

US-09-880-748-2763

Query Match 28.0%; Score 14; DB 9; Length 21;
Best Local Similarity 25.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 YXXXXXXYY 16
DB 6 YDILGYMGSY 17

RESULT 20

US-09-880-748-3010
Sequence 3010, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
FILE REFERENCE: P5523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 3010
LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-3010

Query Match 28.0%; Score 14; DB 9; Length 21;
Best Local Similarity 25.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 YXXXXXXYY 16
DB 5 YDTSGYLGEXY 16

RESULT 21

US-09-895-298-164
Sequence 164, Application US/09895298
Publication No. US20030078405A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 47 Human Secreted Proteins
FILE REFERENCE: P2035P1
CURRENT APPLICATION NUMBER: US/09/895,298
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: 09/591,16
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: PCT/US99/29950
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/113,006
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/112,809
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 231
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 164
LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: SITE
LOCATION: (18)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-895-298-164

Query Match 28.0%; Score 14; DB 9; Length 21;
Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
DB 4 PSSVY 8

RESULT 22

US-10-150-111-174
Sequence 174, Application US/10150111
Publication No. US20030078386A1
GENERAL INFORMATION:
APPLICANT: Rubin et al.
TITLE OF INVENTION: Secreted Protein HPEAD48
FILE REFERENCE: P2018P1D1
CURRENT APPLICATION NUMBER: US/10/150,111
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 09/288,143
PRIOR FILING DATE: 1999-04-08
PRIOR APPLICATION NUMBER: PCT/US98/21142
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/061,463
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,529
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/071,498
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,527
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,536
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,532
PRIOR FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 219
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 174
LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens
US-10-150-111-174

Query Match 28.0%; Score 14; DB 9; Length 21;
Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
DB 17 PNNGF 21

RESULT 23

US-09-879-228-9
Sequence 9, Application US/09879228
Patent No. US20010041350A1
GENERAL INFORMATION:
APPLICANT: Wei et al.
TITLE OF INVENTION: Human DNA Ligase III
FILE REFERENCE: PFI61D2
CURRENT APPLICATION NUMBER: US/09/879,228
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 09/054,775
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: US 08/464,402
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: PCT/US95/03939
PRIOR FILING DATE: 1995-03-31

NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens
US-09-879-228-9

Query Match 28.0%; Score 14; DB 10; Length 21;
Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
11 :
DB 3 PNGMF 7

RESULT 24
US-09-864-761-40485
Sequence 40485, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 40485
LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: MAP TO AC011930.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
OTHER INFORMATION: EST_HUMAN HIT: AAA03053.1, EVALUATE 4.20e-01
US-09-864-761-40485

Query Match 28.0%; Score 14; DB 10; Length 21;
Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
11 :
DB 9 PNGSH 13

RESULT 25
US-08-424-550B-341
Sequence 341, Application US/08424550B
Patent No. US20020119447A1
GENERAL INFORMATION:

APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUDERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 341:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-424-550B-341

Query Match 26.0%; Score 13; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
11
Db 16 PN 17

RESULT 26

US-10-007-270-29
; Sequence 29, Application US/10007270
; Patent No. US20020160954A1
; GENERAL INFORMATION:
; APPLICANT: Hageman, Gregory S.
; APPLICANT: Kuehn, Markus H.
; TITLE OF INVENTION: University of Iowa Research Foundation
; FILE REFERENCE: 020618-000120US
; CURRENT APPLICATION NUMBER: US/10/007,270
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/430,195
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 09/183,972
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: Rat IPM 200 N-terminal amino acid sequence
US-10-007-270-29

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
11
Db 5 PN 6

RESULT 27

US-09-310-113-19
; Sequence 19, Application US/09310113
; Patent No. US20020168744A1
; GENERAL INFORMATION:
; APPLICANT: BRUNSTEDT, Janne
; APPLICANT: CHRISTENSEN, Tove Martel Ida Else
; TITLE OF INVENTION: AMINO ACID SEQUENCE
; FILE REFERENCE: 076883/110
; CURRENT APPLICATION NUMBER: US/09/310,113
; CURRENT FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: GB 9810159.5
; PRIOR FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence affecting activity of a PME
US-09-310-113-19

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
11
Db 12 PN 13

RESULT 28

US-09-736-457-1843
; Sequence 1843, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 1843
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-1843

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
11
Db 18 PN 19

RESULT 29

US-09-736-457-1844
; Sequence 1844, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 1844
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-1844

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
11
Db 10 PN 11

RESULT 30
US-09-736-457-1845
; Sequence 1845, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darriek
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aihun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736.457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1845
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-1845

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
11
DB 2 PN 3

RESULT 31
US-09-902-941-1843
; Sequence 1843, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darriek
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902.941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1843
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-941-1843

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2

DB 18 PN 19

RESULT 32
US-09-902-941-1844
; Sequence 1844, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darriek
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902.941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1844
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-941-1844

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
11
DB 10 PN 11

RESULT 33
US-09-902-941-1845
; Sequence 1845, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darriek
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902.941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1845
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-941-1845

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
11
Db 2 PN 3

RESULT 34
US-10-001-876-189
; Sequence 189, Application US/10001876
; Patent No. US20020177140A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Cafierkey, Robert
; APPLICANT: Ali, Shujath
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
; FILE REFERENCE: DEX-0285
; CURRENT APPLICATION NUMBER: US/10/001,876
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,186
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 189
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-876-189

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
11
Db 9 PN 10

RESULT 35
US-09-795-211-3
; Sequence 3, Application US/09795211
; Publication No. US20020183226A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Kasturi, Chandrika
; APPLICANT: Mandstrat, Mark E.
; APPLICANT: Song, Brian X.
; TITLE OF INVENTION: LIQUID DETERGENT COMPOSITION EXHIBITING ENHANCED a-AMYLASE ENZY
; FILE REFERENCE: STABILITY
; CURRENT APPLICATION NUMBER: US/09/795,211
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 20
; TYPE: PRT
; ORGANISM: akaliiphilicobacillus
US-09-795-211-3

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
11
Db 18 PN 19

RESULT 36
US-09-973-025-57
; Sequence 57, Application US/09973025
; Publication No. US20020182706A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: BOSMAN, FONS
; APPLICANT: DE MARTYNOFF, GUY
; APPLICANT: BUYSSE, MARIE-ANGE

; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
; PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/973,025
; FILING DATE: 10-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/612,973
; FILING DATE: 11-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1487-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-973-025-57

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
11
Db 16 PN 17

RESULT 37
US-09-973-025-58
; Sequence 58, Application US/09973025
; Publication No. US20020182706A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: BOSMAN, FONS
; APPLICANT: DE MARTYNOFF, GUY
; APPLICANT: BUYSSE, MARIE-ANGE
; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
; PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHAYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON

STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/09/973,025
FILING DATE: 10-Oct-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-973-025-58

Query Match
Best Local Similarity 26.0%; Score 13; DB 9; Length 20;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
11
DB 4 PN 5

RESULT 38
US-10-012-896-495
Sequence 495, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Mantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27

CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 495
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-10-012-896-495

Query Match
Best Local Similarity 26.0%; Score 13; DB 9; Length 20;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
11
DB 18 PN 19

RESULT 39
US-10-042-141-83
Sequence 83, Application US/10042141
Publication No. US20020183503A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 26 Human secreted proteins
FILE REFERENCE: P2040P1
CURRENT APPLICATION NUMBER: US/10/042,141
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/726,643
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/15187
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 60/137,725
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 83
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-141-83

Query Match
Best Local Similarity 26.0%; Score 13; DB 9; Length 20;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
11
DB 17 PN 18

RESULT 40
US-09-895-793-495
Sequence 495, Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepner, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurral, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 495
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-09-895-793-495

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
11
Db 18 PN 19

RESULT 41
US-09-895-814-495
Sequence 495, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepner, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurral, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 495
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Made in a lab
US-09-895-814-495

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
11
Db 18 PN 19

RESULT 42
US-09-849-626-1843
Sequence 1843, Application US/09849626
Publication No. US20020197669A1
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya
APPLICANT: Fanger, Gary
APPLICANT: Wang, Aljun
APPLICANT: Wang, Tonglong
APPLICANT: Switzer, Anne
APPLICANT: McNeill, Patricia
APPLICANT: Clapper, Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C16
CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 1926
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1843.
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-849-626-1843

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
11
Db 18 PN 19

RESULT 43
US-09-849-626-1844
Sequence 1844, Application US/09849626
Publication No. US20020197669A1
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya
APPLICANT: Fanger, Gary
APPLICANT: Wang, Aljun
APPLICANT: Wang, Tonglong
APPLICANT: Switzer, Anne
APPLICANT: McNeill, Patricia
APPLICANT: Clapper, Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C16
CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 1926
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1844
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-849-626-1844

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
DB 10 PN 11

RESULT 44

US-09-849-626-1845
; Sequence 1845, Application US/09849626
; Publication No. US20020197669A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya
; APPLICANT: Bangur, Gary
; APPLICANT: Wang, Aljun
; APPLICANT: Wang, Tonglong
; APPLICANT: Switzer, Anne
; APPLICANT: McNeill, Patricia
; APPLICANT: Clapper, Jonathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C16
; CURRENT APPLICATION NUMBER: US/09/849,626
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1845
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-626-1845

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
DB 2 PN-3

RESULT 45

US-09-774-639-366
; Sequence 366, Application US/09774639
; Publication No. US20030003555A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 366
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-639-366

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 40.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 PNXXY 5
DB 2 PQIAY 6

RESULT 46
US-09-863-054-21
; Sequence 21, Application US/09863054
; Publication No. US20030021809A1
; GENERAL INFORMATION:

APPLICANT: Chisari, Francis V.
TITLE OF INVENTION: Peptides for Inducing Cytotoxic T
Lymphocyte Responses to Hepatitis B Virus
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/863,054
FILING DATE: 21-May-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,898
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 08/024,120
FILING DATE: 26-FEB-1993
APPLICATION NUMBER: US 08/396,283
FILING DATE: 27-FEB-1995
APPLICATION NUMBER: US 08/463,486
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lockyer, Jean M.
REGISTRATION NUMBER: 44,879
REFERENCE/DOCKET NUMBER: 014740-000421US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-863-054-21

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PN 2
DB 16 PN 17

RESULT 47

US-09-272-975-14
; Sequence 14, Application US/09272975
; Publication No. US20030027774A1
; GENERAL INFORMATION:
; APPLICANT: Hendrickson, Ronald C.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: TUBERCULOSIS ANTIGENS AND METHODS
; FILE REFERENCE: 210121.474
; CURRENT APPLICATION NUMBER: US/09/272,975
; CURRENT FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: PRT

ORGANISM: Mycobacterium tuberculosis
US-09-272-975-14

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 50.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NXXY 5
DB 17 NTTY 20

RESULT 48

US-09-969-663-6
Sequence 6, Application US/09969663
Publication No. US20030027753A1
GENERAL INFORMATION:
APPLICANT: FAM, Chark Shing
TITLE OF INVENTION: BONE STIMULATING FACTOR
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/969,663
FILING DATE: 04-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/986,627
FILING DATE: 1999-07-22

ATTORNEY/AGENT INFORMATION:
NAME: Maebius, Stephen B.
REGISTRATION NUMBER: 35,264
REFERENCE/DOCKET NUMBER: 79997/119
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: peptide
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-969-663-6

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 17 PN 18

RESULT 49

US-09-899-303-57
Sequence 57, Application US/09899303
Publication No. US20030036110A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
BOSMAN, FONS
DE MARTYNOFF, GUY

BUYS, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE

NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,303
FILING DATE: 06-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996

ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-899-303-57

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PN 2
DB 16 PN 17

RESULT 50

US-09-899-303-58
Sequence 58, Application US/09899303
Publication No. US20030036110A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
BOSMAN, FONS
DE MARTYNOFF, GUY
BUYS, MARIE-ANGE

TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)

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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/899,303
;; FILING DATE: 06-Jul-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/612,973
;; FILING DATE: 11-MAR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BYRNE, THOMAS E.
;; REGISTRATION NUMBER: 32,205
;; REFERENCE/DOCKET NUMBER: 1487-10
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 816-4000
;; TELEFAX: (703) 816-4100
;; INFORMATION FOR SEQ ID NO: 58:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-899-303-58

Query Match 26.0%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PN 2
11
Db 4 PN 5

Search completed: June 11, 2003, 07:58:29
Job time : 245 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 11, 2003, 07:42:24 ; Search time 25 Seconds
(without alignments)
24.715 Million cell updates/sec

Title: US-09-883-727a-127
Perfect score: 50
Sequence: 1 PNMXXXXXXXXXXXXXXXXX 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 9379

Minimum DB seq length: 20
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCRTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	38.0	20	3	US-08-467-023-52
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3	18	36.0	21	1	US-07-657-769B-35
4	18	36.0	21	1	US-08-087-423-5
5	18	36.0	21	1	US-07-789-184-80
6	18	36.0	21	1	US-08-475-263-80
7	18	36.0	21	1	US-08-485-886-80
8	18	36.0	21	2	US-08-477-362-80
9	18	36.0	21	2	US-08-477-134-80
10	18	36.0	21	3	US-08-473-489A-80
11	18	36.0	21	3	US-08-485-695-80
12	18	36.0	21	4	US-08-018-760-80
13	16	32.0	20	1	US-08-383-013A-19
14	16	32.0	20	2	US-08-564-972-15
15	15	30.0	20	1	US-08-382-013A-20
16	15	30.0	20	1	US-08-321-625-50
17	15	30.0	20	4	US-08-612-973-86
18	15	30.0	20	4	US-09-181-083-50
19	15	30.0	20	4	US-08-927-597-86
20	14	28.0	20	1	US-08-318-747-1
21	14	28.0	20	1	US-08-318-747-2
22	14	28.0	20	1	US-08-382-013A-4
23	14	28.0	20	1	US-08-460-874A-23
24	14	28.0	20	1	US-08-460-874A-24
25	14	28.0	20	2	US-08-480-190-35
26	14	28.0	20	2	US-08-480-190-53
27	14	28.0	20	2	US-08-388-883B-23

28	14	28.0	20	2	US-08-388-883B-24	Sequence 24, Appl
29	14	28.0	20	2	US-08-637-759B-230	Sequence 220, App
30	14	28.0	20	2	US-08-488-379-35	Sequence 35, Appl
31	14	28.0	20	2	US-08-488-379-53	Sequence 53, Appl
32	14	28.0	20	2	US-08-603-753D-6	Sequence 6, Appl
33	14	28.0	20	2	US-08-934-915-154	Sequence 154, App
34	14	28.0	20	2	US-08-934-915-155	Sequence 155, App
35	14	28.0	20	2	US-08-107-676-21	Sequence 21, Appl
36	14	28.0	20	3	US-08-871-355A-230	Sequence 230, App
37	14	28.0	20	4	US-08-462-211A-23	Sequence 23, Appl
38	14	28.0	20	4	US-08-462-211A-24	Sequence 24, Appl
39	14	28.0	20	4	US-09-099-753-6	Sequence 6, Appl
40	14	28.0	20	4	US-08-602-999A-159	Sequence 159, App
41	14	28.0	20	4	US-09-201-945-230	Sequence 230, App
42	14	28.0	20	4	US-09-500-124-159	Sequence 159, App
43	14	28.0	20	5	PCT-US93-07545-35	Sequence 35, Appl
44	14	28.0	20	5	PCT-US93-07545-53	Sequence 53, Appl
45	14	28.0	21	1	US-08-460-874A-25	Sequence 25, Appl
46	14	28.0	21	2	US-08-464-402-9	Sequence 9, Appl
47	14	28.0	21	2	US-08-388-883B-25	Sequence 25, Appl
48	14	28.0	21	2	US-08-679-635A-9	Sequence 9, Appl
49	14	28.0	21	3	US-08-293-728-7	Sequence 7, Appl
50	14	28.0	21	4	US-08-462-211A-25	Sequence 25, Appl
51	14	28.0	21	4	US-09-401-476-5	Sequence 5, Appl
52	14	28.0	21	4	US-09-421-868-7	Sequence 7, Appl
53	14	28.0	21	4	US-09-054-775C-9	Sequence 9, Appl
54	14	28.0	21	4	US-09-419-163-9	Sequence 9, Appl
55	14	28.0	21	4	US-09-288-143-174	Sequence 174, App
56	14	28.0	21	6	5433940-21	Patent No. 5433940
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59	13	26.0	20	1	US-07-614-443A-4	Sequence 4, Appl
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61	13	26.0	20	1	US-08-103-742-15	Sequence 15, Appl
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66	13	26.0	20	1	US-08-052-205-12	Sequence 12, Appl
67	13	26.0	20	1	US-08-052-205-19	Sequence 19, Appl
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71	13	26.0	20	1	US-08-218-025A-35	Sequence 35, Appl
72	13	26.0	20	1	US-08-218-025A-56	Sequence 56, Appl
73	13	26.0	20	1	US-08-399-646-10	Sequence 10, Appl
74	13	26.0	20	1	US-08-477-383-18	Sequence 18, Appl
75	13	26.0	20	1	US-08-487-174-10	Sequence 10, Appl
76	13	26.0	20	1	US-08-487-174-18	Sequence 18, Appl
77	13	26.0	20	1	US-07-951-715A-75	Sequence 75, Appl
78	13	26.0	20	1	US-07-678-974D-7	Sequence 7, Appl
79	13	26.0	20	1	US-07-678-974D-6	Sequence 6, Appl
80	13	26.0	20	1	US-08-480-750-18	Sequence 18, Appl
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82	13	26.0	20	1	US-08-241-054-84	Sequence 84, Appl
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84	13	26.0	20	1	US-08-390-156A-72	Sequence 72, Appl
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86	13	26.0	20	1	US-08-291-859-2	Sequence 2, Appl
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88	13	26.0	20	1	US-08-595-974-12	Sequence 12, Appl
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90	13	26.0	20	1	US-08-440-861-12	Sequence 12, Appl
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103	13	26.0	20	1	US-08-199-508-8	Sequence 8, App1
104	13	26.0	20	1	US-08-199-508-9	Sequence 9, App1
105	13	26.0	20	1	US-08-439-817-64	Sequence 64, App1
106	13	26.0	20	1	US-08-439-817-72	Sequence 72, App1
107	13	26.0	20	1	US-08-481-676-4	Sequence 4, App1
108	13	26.0	20	1	US-08-488-252-26	Sequence 26, App1
109	13	26.0	20	1	US-08-040-548-63	Sequence 63, App1
110	13	26.0	20	1	US-08-401-136-2	Sequence 2, App1
111	13	26.0	20	1	US-08-484-135-50	Sequence 50, App1
112	13	26.0	20	1	US-08-484-135-57	Sequence 57, App1
113	13	26.0	20	1	US-08-484-135-91	Sequence 91, App1
114	13	26.0	20	1	US-08-484-635-223	Sequence 223, App
115	13	26.0	20	1	US-08-484-635-229	Sequence 229, App
116	13	26.0	20	1	US-08-466-344-63	Sequence 63, App1
117	13	26.0	20	1	US-08-416-950-10	Sequence 10, App1
118	13	26.0	20	1	US-08-455-633A-2	Sequence 2, App1
119	13	26.0	20	1	US-08-485-508-84	Sequence 84, App1
120	13	26.0	20	1	US-08-485-508-92	Sequence 92, App1
121	13	26.0	20	1	US-08-614-935-9	Sequence 9, App1
122	13	26.0	20	1	US-08-614-935-10	Sequence 10, App1
123	13	26.0	20	1	US-08-039-364-3	Sequence 3, App1
124	13	26.0	20	2	US-08-446-803-3	Sequence 3, App1
125	13	26.0	20	2	US-08-480-190-56	Sequence 56, App1
126	13	26.0	20	2	US-08-480-190-244	Sequence 244, App
127	13	26.0	20	2	US-08-961-240-10	Sequence 10, App1
128	13	26.0	20	2	US-08-484-631-223	Sequence 223, App
129	13	26.0	20	2	US-08-605-501-10	Sequence 10, App1
130	13	26.0	20	2	US-08-139-609-11	Sequence 11, App1
131	13	26.0	20	2	US-08-564-972-32	Sequence 32, App1
132	13	26.0	20	2	US-08-484-530-10	Sequence 10, App1
133	13	26.0	20	2	US-08-861-837-3	Sequence 3, App1
134	13	26.0	20	2	US-08-459-448A-75	Sequence 75, App1
135	13	26.0	20	2	US-08-487-074-6	Sequence 6, App1
136	13	26.0	20	2	US-08-488-379-56	Sequence 56, App1
137	13	26.0	20	2	US-08-146-028-33	Sequence 33, App1
138	13	26.0	20	2	US-08-146-028-172	Sequence 172, App
139	13	26.0	20	2	US-08-447-430A-32	Sequence 32, App1
140	13	26.0	20	2	US-08-871-074-14	Sequence 14, App1
141	13	26.0	20	2	US-08-469-830-10	Sequence 10, App1
142	13	26.0	20	2	US-08-934-915-25	Sequence 25, App1
143	13	26.0	20	2	US-08-934-915-44	Sequence 44, App1
144	13	26.0	20	2	US-08-934-915-123	Sequence 123, App
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147	13	26.0	20	2		
148	13	26.0	20	2		
149	13	26.0	20	2		
150	13	26.0	20	2		

ALIGNMENTS

RESULT 1
Sequence 52, Application US/08467023
Patent No. 6090386
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
NUMBER OF SEQUENCES: Japanese Cedar Pollen
CORRESPONDENCE ADDRESS: 261

ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-467-023-52

Query Match 38.0%; Score 19; DB 3; Length 20;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
DB 11 PNEYS 15

RESULT 2
Sequence 53, Application US/08467023
Patent No. 6090386
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
NUMBER OF SEQUENCES: Japanese Cedar Pollen
CORRESPONDENCE ADDRESS: 261
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remiliard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-467-023-53

Query Match 38.0%; Score 19; DB 3; Length 20;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
1111
DB 1 PNEY 5

RESULT 3
US-07-657-769B-35
Sequence 35, Application US/07657769B
Patent No. 5256766
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED
TITLE OF INVENTION: PHARMACEUTICALS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: IRELL & MANELLA
STREET: 545 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/657,769B
FILING DATE: 19910219
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0502.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-657-769B-35

Query Match 36.0%; Score 18; DB 1; Length 21;

Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
1111
DB 11 PNDKY 15

RESULT 4
US-08-087-423-5
Sequence 5, Application US/08087423
Patent No. 5455228
GENERAL INFORMATION:
APPLICANT: Collier, Barry S.
APPLICANT: Prestwich, Glenn D.
TITLE OF INVENTION: Peptidase Resistant Thrombin
TITLE OF INVENTION: Receptor Thrombin Ligand
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: United States of America
ZIP: 11753
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 5.25 inch, 360 KBL
COMPUTER: IBM XT compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,423
FILING DATE: 02-July-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA: No. 5455228e
ATTORNEY/AGENT INFORMATION:
NAME: MORRIS, ARLENE D.
REGISTRATION NUMBER: 32,657
REFERENCE/DOCKET NUMBER: 178-150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 Amino Acids
TYPE: Amino Acid
TOPOLOGY: linear
MOLECULE TYPE: Peptide
FRAGMENT TYPE: Internal Fragment
US-08-087-423-5

Query Match 36.0%; Score 18; DB 1; Length 21;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
1111
DB 14 PNDKY 18

RESULT 5
US-07-789-184-80
Sequence 80, Application US/07789184
Patent No. 5688768
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
TITLE OF INVENTION: RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road

```

; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,184
; FILING DATE: 19911107
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-07-789-184-80

Query Match          36.0%; Score 18; DB 1; Length 21;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 PNXXY 5
        || |
        11 PNDKY 15

Db      11 PNDKY 15

RESULT 6
US-08-475-263-80
; Sequence 80, Application US/08475263
; Patent No. 575994
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,263
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 80:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-475-263-80

Query Match          36.0%; Score 18; DB 1; Length 21;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 PNXXY 5
        || |
        11 PNDKY 15

Db      11 PNDKY 15

RESULT 7
US-08-485-886-80
; Sequence 80, Application US/08485886
; Patent No. 5798248
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,886
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-485-886-80

Query Match          36.0%; Score 18; DB 1; Length 21;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 PNXXY 5
        || |
        11 PNDKY 15

Db      11 PNDKY 15

RESULT 8
US-08-477-362-80
; Sequence 80, Application US/08477362

```

Patent No. 5849507
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
TITLE OF INVENTION: RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,362
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-477-362-80

Query Match 36.0%; Score 18; DB 2; Length 21;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
DB 11 PNDKY 15

RESULT 9
US-08-477-134-80
Sequence 80, Application US/08477134
Patent No. 5856448
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
TITLE OF INVENTION: RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,134
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-477-134-80

Query Match 36.0%; Score 18; DB 2; Length 21;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
DB 11 PNDKY 15

RESULT 10
US-08-473-489A-80
Sequence 80, Application US/08473489A
Patent No. 6024936
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
TITLE OF INVENTION: RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,489A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/789,184
FILING DATE: 1991-11-07
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid

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STRANDEDNESS: single
TOPOLOGY: linear
US-08-473-489A-80

Query Match
Best Local Similarity 36.0%; Score 18; DB 3; Length 21;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
DB 11 PNDKY 15

RESULT 11
US-08-485-695-80
Sequence 80, Application US/08485695
Patent No. 6124101
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,695
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-695-80

Query Match
Best Local Similarity 36.0%; Score 18; DB 3; Length 21;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
DB 11 PNDKY 15

RESULT 12
US-08-018-760-80
Sequence 80, Application US/08018760
Patent No. 6197541
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
```

```
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/018,760
FILING DATE: 17-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-018-760-80

Query Match
Best Local Similarity 36.0%; Score 18; DB 4; Length 21;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
DB 11 PNDKY 15

RESULT 13
US-08-382-013A-19
Sequence 19, Application US/08382013A
Patent No. 5631222
GENERAL INFORMATION:
APPLICANT: Shibata, Kenji
APPLICANT: Suzawa, Toshiyuki
APPLICANT: Yamasaki, Motoo
APPLICANT: Tanaka, Takeo
APPLICANT: Tsukuda, Koji
APPLICANT: Yamada, Koji
APPLICANT: Ohno, Tetsuji
TITLE OF INVENTION: Endothelin-Antagonizing Peptide
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
```


SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/382,013A
FILING DATE: 10-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 155031/93
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lipfert, Nels T.
REGISTRATION NUMBER: 25888
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-819-8200
TELEFAX: 212-354-8113
TELEX: 233188
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-382-013A-19

Query Match 32.0%; Score 16; DB 1; Length 20;
Best Local Similarity 27.3%; Pred. No. 7.5e+02;
Matches 3; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 PNXVXXXXXXXXX 11
I: | |
DB 8 PDWVYFAHLNY 18

RESULT 14
US-08-564-972-15
Sequence 15, Application US/08564972
Patent No. 5843462
GENERAL INFORMATION:
APPLICANT: Conli-Fine, B. M.
TITLE OF INVENTION: DIPHTHERIA TOXIN EPTOPES
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,972
FILING DATE: 30-NOV-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 600,344US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-564-972-15

Query Match 32.0%; Score 16; DB 2; Length 20;
Best Local Similarity 25.0%; Pred. No. 7.5e+02;
Matches 3; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 YXXXXXXXXXX 16
I: | |
DB 4 YSTDNKYDAGY 15

RESULT 15
US-08-382-013A-20
Sequence 20, Application US/08382013A
Patent No. 5631222
GENERAL INFORMATION:
APPLICANT: Shibata, Kenji.
APPLICANT: Suzawa, Toshiyuki
APPLICANT: Yamasaki, Motoo
APPLICANT: Tanaka, Takeo
APPLICANT: Tsukuda, Eiji
APPLICANT: Yamada, Koji
APPLICANT: Ohno, Tetsuji
TITLE OF INVENTION: Endothelin-Antagonizing Peptide
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/382,013A
FILING DATE: 10-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 155031/93
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lipfert, Nels T.
REGISTRATION NUMBER: 25888
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-819-8200
TELEFAX: 212-354-8113
TELEX: 233188
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-382-013A-20

Query Match 30.0%; Score 15; DB 1; Length 20;
Best Local Similarity 27.3%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 PNXVXXXXXXXXX 11
I: | |
DB 8 PDWVYFAHLNY 18

RESULT 16
US-08-321-625-50
; Sequence 50, Application US/08321625
; Patent No. 5639860
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Takeo
; APPLICANT: MORISHITA, Yoshikazu
; APPLICANT: MAKINO, Mika
; APPLICANT: CHIBA, Shigeru
; APPLICANT: KAWAMOTO, Isao
; APPLICANT: TSUKUDA, Ei-ji
; APPLICANT: YOSHIDA, Mayumi
; APPLICANT: BANDO, Chieko
; APPLICANT: YAMAGUCHI, Kazuo
; TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
; STREET: 1300 No. 5639860th Seventeenth Street, Suite 1800
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/321,625
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TERRY, David T.
; REGISTRATION NUMBER: 20,178
; REFERENCE/DOCKET NUMBER: 506.32366Px1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-312-6600
; TELEFAX: 703-312-6666
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-321-625-50

Query Match 30.0%; Score 15; DB 1; Length 20;
Best Local Similarity 27.3%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 PNXYYXXXXXX 11
1: |
8 PDWYFAFFNY 18

DB

RESULT 17
US-08-612-973-86
; Sequence 86, Application US/08612973
; Patent No. 6150134
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: BOSMAN, FONS
; APPLICANT: DE MARTYNOFF, GUY
; APPLICANT: BUYSSE, MARIE-ANGE
; TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE

;; TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
;; NUMBER OF SEQUENCES: 111
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: NIXON & VANDERHVE P.C.
;; STREET: 1100 NORTH GLEBE ROAD
;; CITY: ARLINGTON
;; STATE: VIRGINIA
;; COUNTRY: U.S.A.
;; ZIP: 22201-4714
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/612,973
;; FILING DATE: 11-MAR-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BYRNE, THOMAS E.
;; REGISTRATION NUMBER: 32,205
;; REFERENCE/DOCKET NUMBER: 1487-10
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 816-4000
;; TELEFAX: (703) 816-4100
;; INFORMATION FOR SEQ ID NO: 86:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-612-973-86

Query Match 30.0%; Score 15; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXYY 5
1: |
8 PDATY 12

DB

RESULT 18
US-09-181-083-50
; Sequence 50, Application US/09181083
; Patent No. 6194195
; GENERAL INFORMATION:
; APPLICANT: TANAKA, Takeo
; APPLICANT: MORISHITA, Yoshikazu
; APPLICANT: MAKINO, Mika
; APPLICANT: CHIBA, Shigeru
; APPLICANT: KAWAMOTO, Isao
; APPLICANT: TSUKUDA, Ei-ji
; APPLICANT: YOSHIDA, Mayumi
; APPLICANT: BANDO, Chieko
; APPLICANT: YAMAGUCHI, Kazuo
; APPLICANT: MATSUDA, Yuzuru
; TITLE OF INVENTION: ENDOTHELIN-ANTAGONIZING PEPTIDE
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANTONELLI, TERRY, STOUT & KRAUS
; STREET: 1300 No. 6194195th Seventeenth Street, Suite 1800
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/181,083
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/321,625
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: TERRY, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 506.32366PX1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-09-181-083-50

Query Match 30.0%; Score 15; DB 4; Length 20;
Best Local Similarity 27.3%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 PNXXYXXXXXX 11
Db 8 PDWYFAFENY 18

RESULT 19
US-08-927-597-86
Sequence 86, Application US/08927597
Patent No. 6245503
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEEFT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 86:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-927-597-86

Query Match 30.0%; Score 15; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
Db 8 PDATY 12

RESULT 20
US-08-318-747-1
Sequence 1, Application US/08318747
Patent No. 5582825
GENERAL INFORMATION:
APPLICANT: SAKAGUCHI, Kenji
APPLICANT: MURATA, Kosaku
APPLICANT: KIMURA, Akira
APPLICANT: YONEMOTO, Yoshimasa
APPLICANT: YAMAGUCHI, Hisako
APPLICANT: OKAYAMA, Kenichi
APPLICANT: YAMASHITA, Tetsuo
APPLICANT: ABE, Shiro
APPLICANT: HISANO, Tomohiro
APPLICANT: NISHIMURA, Minoru
TITLE OF INVENTION: THERAPEUTIC MEDICINE FOR CYSTIC FIBROSIS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westernman, Hattori, Mclelland &
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,747
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00227
FILING DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 940908
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
TELEX: 440142
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-747-1

Query Match 28.0%; Score 14; DB 1; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PNXXY 5
DB 11 PTASY 15

RESULT 21

US-08-318-747-2
; Sequence 2, Application US/08318747
; Patent No. 5582825

GENERAL INFORMATION:

APPLICANT: SAKAGUCHI, Kenji
APPLICANT: MURATA, Kosaku
APPLICANT: KIMURA, Akira
APPLICANT: YONEMOTO, Yoshimasa
APPLICANT: YAMAGUCHI, Hisako
APPLICANT: OKAYAMA, Kenichi
APPLICANT: YAMASHITA, Tetsuo
APPLICANT: ABE, Shiro
APPLICANT: HISANO, Tomohiro
APPLICANT: NISHIMURA, Minoru
TITLE OF INVENTION: THERAPEUTIC MEDICINE FOR CYSTIC FIBROSIS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westernman, Hattori, Mclelland &
ADDRESSEE: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 In, 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/318,747
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00227
FILING DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 940908
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
TELEX: 440142

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-747-2

Query Match 28.0%; Score 14; DB 1; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PNXXY 5
DB 11 PTASY 15

RESULT 22
US-08-382-013A-4
; Sequence 4, Application US/08382013A
; Patent No. 5631222
; GENERAL INFORMATION:

APPLICANT: Shibata, Kenji
APPLICANT: Suzawa, Toshiyuki
APPLICANT: Yamasaki, Motoo
APPLICANT: Tanaka, Takeo
APPLICANT: Tsukuda, Eiji
APPLICANT: Yamada, Koji
APPLICANT: Ohno, Tetsuji
TITLE OF INVENTION: Endothelin-Antagonizing Peptide
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/382,013A
FILING DATE: 10-FEB-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 155031/93
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:

NAME: Lippert, Nels T.

REGISTRATION NUMBER: 25888

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-819-8200

TELEFAX: 212-354-8113

TELEX: 233188

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-382-013A-4

Query Match 28.0%; Score 14; DB 1; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
DB 8 PDVAVY 12

RESULT 23

US-08-460-874A-23
; Sequence 23, Application US/08460874A
; Patent No. 5744298

GENERAL INFORMATION:

APPLICANT: Stuber, Werner
APPLICANT: Wleczorek, Leszek
APPLICANT: Ziegelmaler, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,874A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05552-1210-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-874A-23

Query Match 28.0%; Score 14; DB 1; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
|: |
Db 15 PHLAY 19

RESULT 24
US-08-460-874A-24
Sequence 24, Application US/08460874A
Patent No. 5744298
GENERAL INFORMATION:
APPLICANT: Studer, Werner
APPLICANT: Wlaczorek, Leszek
APPLICANT: Ziegelmair, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,874A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7

FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05552-1210-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-874A-24

Query Match 28.0%; Score 14; DB 1; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
|: |
Db 12 PHLAY 16

RESULT 25
US-08-480-190-35
Sequence 35, Application US/08480190
Patent No. 5827516
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 50z or 555x
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

US-08-480-190-35

Query Match 28.0%; Score 14; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
11 :
DB 7 PNNTH 11

RESULT 26

US-08-480-190-53
; Sequence 53, Application US/08480190
; Patent No. 5827516

; GENERAL INFORMATION:

; APPLICANT: Robert G. Urban

; APPLICANT: Roman M. Chicz

; APPLICANT: Darío A. A. Vignali

; APPLICANT: Mary L. Hedley

; APPLICANT: Lawrence J. Stern

; APPLICANT: Jack L. Strominger

; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES

; NUMBER OF SEQUENCES: 274

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; OPERATING SYSTEM: MS-DOS (Version 5.0)

; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/480,190

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/077,255

; FILING DATE: June 15, 1993

; APPLICATION NUMBER: 07/925,460

; FILING DATE: August 11, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Clark, Paul T.

; REGISTRATION NUMBER: 30,162

; REFERENCE/DOCKET NUMBER: 00246/168001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; US-08-480-190-53

Query Match 28.0%; Score 14; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
1 :
DB 14 PDAEY 18

RESULT 27

US-08-388-883B-23
; Sequence 23, Application US/0838883B

; Patent No. 5859185

; GENERAL INFORMATION:

; APPLICANT: ST BER, Werner

; APPLICANT: WIECZOREK, Leszek

; APPLICANT: ZIEGELMAIER, Robert

; TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finegan, Henderson, Farabow, Garrett &

; STREET: 1300 I Street, N.W., Suite 700

; CITY: Washington,

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/388,883B

; FILING DATE: 13-FEB-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/300,305,

; FILING DATE: 23-FEB-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/936,219

; FILING DATE: 27-AUG-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P4128684.7

; FILING DATE: 29-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Forman, David S.

; REGISTRATION NUMBER: 33,694

; REFERENCE/DOCKET NUMBER: 5552-1210-02000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-408-4400

; TELEFAX: 202-408-4400

; INFORMATION FOR SRO ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-388-883B-23

Query Match 28.0%; Score 14; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
1 :
DB 15 PHLAY 19

RESULT 28

US-08-388-883B-24
; Sequence 24, Application US/0838883B

; Patent No. 5859185

; GENERAL INFORMATION:

; APPLICANT: ST BER, Werner

; APPLICANT: WIECZOREK, Leszek

; APPLICANT: ZIEGELMAIER, Robert

; TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finegan, Henderson, Farabow, Garrett &

; STREET: 1300 I Street, N.W., Suite 700

CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3115
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,883B
FILING DATE: 13-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,305
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 5552-1210-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4000
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-388-883B-24

Query Match 28.0%; Score 14; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
1:
12 PHLAY 16

Db

RESULT 29
US-08-637-759B-230
Sequence 230, Application US/08637759B
Patent No. 5876931
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875

FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 230:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-637-759B-230

Query Match 28.0%; Score 14; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
1:
10 PSSGY 14

Db

RESULT 30
US-08-488-379-35
Sequence 35, Application US/08488379
Patent No. 5880103
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,379
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 20

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-488-379-35

Query Match 28.0%; Score 14; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
DB 7 PNNTH 11

RESULT 31
US-08-488-379-53
Sequence 53, Application US/08488379
Patent No. 5880103
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Darío A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,379
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-488-379-53

Query Match 28.0%; Score 14; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
DB 14 PDAEY 18

RESULT 32
US-08-603-753D-6
Sequence 6, Application US/08603753D
Patent No. 5891857
GENERAL INFORMATION:
APPLICANT: HOLT, JEFFREY T.
APPLICANT: JENSEN, ROY A.
APPLICANT: PAGE, DAVID L.
APPLICANT: KING, MARY-CLAIRE
APPLICANT: SZABO, CSILLA I.
APPLICANT: JETTON, THOMAS L.
APPLICANT: ROBINSON-BENION, CHERYL L.
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/603,753D
FILING DATE: 20 FEB 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/373,799
FILING DATE: 17 JAN 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens sapiens
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
CELL TYPE: normal breast tissue
CELL LINE: HMEC
ORGANELLE: no
FEATURE:
NAME/KEY: BRCA1 C-20 antigen
LOCATION: 1844 to 1863
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
PAGES:

DATE: RELEVANT RESIDUES IN SEQ ID NO: 6
US-08-603-753D-6

Query Match 28.0%; Score 14; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
11
Db 16 PNRHH 20

RESULT 33
US-08-934-915-154
Sequence 154, Application US/08934915
Patent No. 5932412

GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P. A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foulch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-154

Query Match 28.0%; Score 14; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
11
Db 16 PNRHH 20

RESULT 34
US-08-934-915-155
Sequence 155, Application US/08934915

Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P. A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foulch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 155:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-155

Query Match 28.0%; Score 14; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
11
Db 16 PNRHH 5

RESULT 35
US-08-107-676-21
Sequence 21, Application US/08107676
Patent No. 5953356

GENERAL INFORMATION:
APPLICANT: Content, Jean
APPLICANT: Dewit, Lucas
TITLE OF INVENTION: Mycobacterium Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding Them for Diagnosis and Control of
TITLE OF INVENTION: Tuberculosis
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5955356west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,676
FILING DATE: 04-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP92/00268
FILING DATE: 07-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91400388.4
FILING DATE: 14-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchuk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076,89USWO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-107-676-21

Query Match 28.0%; Score 14; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. NO. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PNXXY 5
11;
Db 7 PNGTH 11

RESULT 36
US-08-871-355A-230
Sequence 230, Application US/08871355A
Patent No. 6015669
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,355A
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101 CON
TELECOMMUNICATION INFORMATION:

TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 230:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-871-355A-230

Query Match 28.0%; Score 14; DB 3; Length 20;
Best Local Similarity 40.0%; Pred. NO. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PNXXY 5
11;
Db 10 PSSGY 14

RESULT 37
US-08-462-211A-23
Sequence 23, Application US/08462211A
Patent No. 6143493
GENERAL INFORMATION:
APPLICANT: Stuber, Werner
APPLICANT: Wiczorek, Leszek
APPLICANT: Ziegelmaler, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,211A
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/388,883
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,305
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 5552.1210-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-462-211A-23

Query Match 28.0%; Score 14; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
1: 1
DB 15 PHLAY 19

RESULT 38

US-08-462-211A-24
Sequence 24, Application US/08462211A
Patent No. 6143493
GENERAL INFORMATION:
APPLICANT: Studer, Werner
APPLICANT: Wleczorek, Leszek
APPLICANT: Ziegelmair, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
ADDRESS: Dunner L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,211A
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/388,883
FILING DATE: 13-FEB-1995
APPLICATION DATA:
APPLICATION NUMBER: US 08/300,305
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 5552.1210-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-462-211A-24

Query Match 28.0%; Score 14; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
1: 1
DB 12 PHLAY 16

RESULT 39
US-09-099-753-6
Sequence 6, Application US/0909753
Patent No. 6149903

GENERAL INFORMATION:
APPLICANT: HOLT, JEFFREY T.
APPLICANT: JENSEN, ROY A.
APPLICANT: PAGE, DAVID L.
APPLICANT: KING, MARY-CLAIRE
APPLICANT: SZABO, CSILLA I.
APPLICANT: JETTON, THOMAS L.
APPLICANT: ROBINSON-BENION, CHERYL L.
APPLICANT: THOMPSON, MARILYN E.
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
STREET: BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage

COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1

SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,753
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/603,753

FILING DATE: 20 FEB 1996

APPLICATION NUMBER: U.S. 08/373,799
FILING DATE: 17 JAN 1995

ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.

REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 483-8000
TELEFAX: (919) 419-0383

TELEX:

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 20

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

HYPOTHETICAL: no

ANTI-SENSE: no

ORIGINAL SOURCE:

ORGANISM: Homo sapiens sapiens

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE: adult

TISSUE TYPE: female breast

CELL TYPE: normal breast tissue

CELL LINE: HMEC

ORGANELLE: no

FEATURE:

NAME/KEY: BRCA1 C-20 antigen

LOCATION: 1844 to 1863

IDENTIFICATION METHOD:

OTHER INFORMATION:

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:
VOLUME:
PAGES:
DATE:
RELEVANT RESIDUES IN SEQ ID NO: 6

Query Match 28.0%; Score 14; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
DB 16 PSSHY 20

RESULT 40
US-08-602-999A-159
Sequence 159, Application US/08602999A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 159:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-159

Query Match 28.0%; Score 14; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 PNXXY 5
DB 12 PSSY 16

RESULT 41

US-09-201-945-230

Sequence 230, Application US/09201945
Patent No. 6342215
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 230:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-201-945-230

Query Match 28.0%; Score 14; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
DB 10 PSSGY 14

RESULT 42
US-09-500-124-159
Sequence 159, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 159:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-159

Query Match
Best Local Similarity 28.0%; Score 14; DB 4; Length 20;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 PNNXY 5
Db 12 POSSY 16

RESULT 43
PCT-US93-07545-35
; Sequence 35, Application PC/TUS9307545
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07545
; FILING DATE: 19930811
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-07545-35

Query Match
Best Local Similarity 28.0%; Score 14; DB 5; Length 20;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNNXY 5
Db 7 PNNFH 11

RESULT 44
PCT-US93-07545-53
; Sequence 53, Application PC/TUS9307545
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07545
; FILING DATE: 19930811
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US93-07545-53

Query Match
Best Local Similarity 28.0%; Score 14; DB 5; Length 20;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
1: 1
Db 14 PDAXY 18

RESULT 45
US-08-460-874A-25
Sequence 25, Application US/08460874A
Patent No. 5744298
GENERAL INFORMATION:
APPLICANT: Studer, Werner
APPLICANT: Wiczorek, Leszek
APPLICANT: Ziegelmaier, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,874A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05552-1210-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-874A-25

Query Match 28.0%; Score 14; DB 1; Length 21;
Best Local Similarity 40.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
1: 1
Db 9 PHLAY 13

RESULT 46
US-08-464-402-9
Sequence 9, Application US/08464402
Patent No. 5858705
GENERAL INFORMATION:
APPLICANT: WEI, ET AL.
TITLE OF INVENTION: Human DNA Ligase III
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,402
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03939
FILING DATE: 31 MAR 95
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-388
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-464-402-9

Query Match 28.0%; Score 14; DB 2; Length 21;
Best Local Similarity 40.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PNXXY 5
1: 1
Db 3 PNCMF 7

RESULT 47
US-08-388-883B-25
Sequence 25, Application US/08388883B
Patent No. 5859185
GENERAL INFORMATION:
APPLICANT: ST BER, Werner
APPLICANT: WICZOREK, Leszek
APPLICANT: ZIEGELMAIER, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,883B
FILING DATE: 13-FEB-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,305
FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
PRIOR APPLICATION DATA: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Foiman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 3552-1210-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-388-883B-25

Query Match 28.0%; Score 14; DB 2; Length 21;
Best Local Similarity 40.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
1 :
Db 9 PHLAY 13

RESULT 48
US-08-679-635A-9
Sequence 9, Application US/08679635A
Patent No. 5985643
GENERAL INFORMATION:
APPLICANT: Tomasz, Alexander
APPLICANT: Delencastre, Herminia
TITLE OF INVENTION: AUXILIARY GENES AND PROTEINS OF
TITLE OF INVENTION: METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,635A
FILING DATE: 10-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-679-635A-9

Query Match 28.0%; Score 14; DB 2; Length 21;
Best Local Similarity 40.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
1 :
Db 16 PNGDF 20

RESULT 49
US-08-293-728-7
Sequence 7, Application US/08293728D
Patent No. 6008341
GENERAL INFORMATION:
APPLICANT: Foster, Timothy J.
APPLICANT: McDevitt, Damien L.
TITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene
FILE REFERENCE: 05344.105011
CURRENT APPLICATION NUMBER: US/08/293,728D
CURRENT FILING DATE: 1994-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 21
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-293-728-7

Query Match 28.0%; Score 14; DB 3; Length 21;
Best Local Similarity 40.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNXXY 5
1 :
Db 14 PNILF 18

RESULT 50
US-08-462-211A-25
Sequence 25, Application US/08462211A
Patent No. 6143493
GENERAL INFORMATION:
APPLICANT: Studer, Werner
APPLICANT: Wleczorek, Leszek
APPLICANT: Ziegelmayer, Robert
TITLE OF INVENTION: HCMV-Specific Peptides, Agents Therefor
TITLE OF INVENTION: and the Use Thereof
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
ADDRESSEE: Dunner L.L.P.
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington,
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,211A
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/388,883
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,305

FILING DATE: 23-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/936,219
FILING DATE: 27-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4128684.7
FILING DATE: 29-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 5552.1210-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-462-211A-25

Query Match 28.0%; Score 14; DB 4; Length 21;
Best Local Similarity 40.0%; Pred. No. 2.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 PNXXY 5
| : |
Db 9 PHLAY 13

Search completed: June 11, 2003, 07:44:51
Job time : 28 secs